

Recovering Gene Interactions from Single-Cell Data Usi

Cell

174, 716-729.e27

DOI: [10.1016/j.cell.2018.05.061](https://doi.org/10.1016/j.cell.2018.05.061)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Unsupervised Metric Learning in Presence of Missing Data. , 2018, , .		4
2	Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies. Nature Protocols, 2018, 13, 2742-2757.	5.5	153
3	VIPER: variability-preserving imputation for accurate gene expression recovery in single-cell RNA sequencing studies. Genome Biology, 2018, 19, 196.	3.8	97
4	Single-cell RNA-sequencing reveals transcriptional dynamics of estrogen-induced dysplasia in the ovarian surface epithelium. PLoS Genetics, 2018, 14, e1007788.	1.5	16
5	Comparative Analysis and Refinement of Human PSC-Derived Kidney Organoid Differentiation with Single-Cell Transcriptomics. Cell Stem Cell, 2018, 23, 869-881.e8.	5.2	419
6	ddSeeker: a tool for processing Bio-Rad ddSEQ single cell RNA-seq data. BMC Genomics, 2018, 19, 960.	1.2	22
7	An integrative approach for building personalized gene regulatory networks for precision medicine. Genome Medicine, 2018, 10, 96.	3.6	49
8	Bayesian deep learning for single-cell analysis. Nature Methods, 2018, 15, 1009-1010.	9.0	21
9	Ensemble Estimation of Information Divergence $\hat{\epsilon}$. Entropy, 2018, 20, 560.	1.1	14
10	Learning time-varying information flow from single-cell epithelial to mesenchymal transition data. PLoS ONE, 2018, 13, e0203389.	1.1	18
11	Revealing routes of cellular differentiation by single-cell RNA-seq. Current Opinion in Systems Biology, 2018, 11, 9-17.	1.3	10
12	Co-expression in Single-Cell Analysis: Saving Grace or Original Sin?. Trends in Genetics, 2018, 34, 823-831.	2.9	34
13	Single-Cell Survey of Human Lymphatics Unveils Marked Endothelial Cell Heterogeneity and Mechanisms of Homing for Neutrophils. Immunity, 2019, 51, 561-572.e5.	6.6	149
14	scHinter: imputing dropout events for single-cell RNA-seq data with limited sample size. Bioinformatics, 2020, 36, 789-797.	1.8	16
15	Block HSIC Lasso: model-free biomarker detection for ultra-high dimensional data. Bioinformatics, 2019, 35, i427-i435.	1.8	44
16	RESCUE: imputing dropout events in single-cell RNA-sequencing data. BMC Bioinformatics, 2019, 20, 388.	1.2	30
17	Transcriptional Regulation in the Immune System: One Cell at a Time. Frontiers in Immunology, 2019, 10, 1355.	2.2	12
18	Differential Variation Analysis Enables Detection of Tumor Heterogeneity Using Single-Cell RNA-Sequencing Data. Cancer Research, 2019, 79, 5102-5112.	0.4	23

#	ARTICLE	IF	CITATIONS
19	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. <i>Cell</i> , 2019, 178, 714-730.e22.	13.5	806
20	Computational approaches for characterizing the tumor immune microenvironment. <i>Immunology</i> , 2019, 158, 70-84.	2.0	30
21	Single-Cell Transcriptomics Reveals Spatial and Temporal Turnover of Keratinocyte Differentiation Regulators. <i>Frontiers in Genetics</i> , 2019, 10, 775.	1.1	45
22	A cellular atlas of <i>Pitx2</i> -dependent cardiac development. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	44
23	DeepImpute: an accurate, fast, and scalable deep neural network method to impute single-cell RNA-seq data. <i>Genome Biology</i> , 2019, 20, 211.	3.8	185
24	MetaCell: analysis of single-cell RNA-seq data using K-nn graph partitions. <i>Genome Biology</i> , 2019, 20, 206.	3.8	218
25	Transcriptional Basis of Mouse and Human Dendritic Cell Heterogeneity. <i>Cell</i> , 2019, 179, 846-863.e24.	13.5	359
26	UM171 induces a homeostatic inflammatory-detoxification response supporting human HSC self-renewal. <i>PLoS ONE</i> , 2019, 14, e0224900.	1.1	31
27	Sequencing the Human Brain at Single-Cell Resolution. <i>Current Behavioral Neuroscience Reports</i> , 2019, 6, 197-208.	0.6	5
28	Single-cell sequencing and its applications in head and neck cancer. <i>Oral Oncology</i> , 2019, 99, 104441.	0.8	65
29	Mapping genetic interactions in cancer: a road to rational combination therapies. <i>Genome Medicine</i> , 2019, 11, 62.	3.6	16
31	Data denoising with transfer learning in single-cell transcriptomics. <i>Nature Methods</i> , 2019, 16, 875-878.	9.0	152
32	Network modeling of single-cell omics data: challenges, opportunities, and progresses. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 379-398.	1.1	48
33	Current best practices in single-cell RNA-seq analysis: a tutorial. <i>Molecular Systems Biology</i> , 2019, 15, e8746.	3.2	1,322
34	IL-2 production by self-reactive CD4 thymocytes scales regulatory T cell generation in the thymus. <i>Journal of Experimental Medicine</i> , 2019, 216, 2466-2478.	4.2	62
35	Unified single-cell analysis of testis gene regulation and pathology in five mouse strains. <i>ELife</i> , 2019, 8, .	2.8	102
36	A pooled single-cell genetic screen identifies regulatory checkpoints in the continuum of the epithelial-to-mesenchymal transition. <i>Nature Genetics</i> , 2019, 51, 1389-1398.	9.4	150
37	Tet inactivation disrupts YY1 binding and long-range chromatin interactions during embryonic heart development. <i>Nature Communications</i> , 2019, 10, 4297.	5.8	44

#	ARTICLE	IF	CITATIONS
38	Systems biology approaches to measure and model phenotypic heterogeneity in cancer. <i>Current Opinion in Systems Biology</i> , 2019, 17, 35-40.	1.3	17
39	Hippo pathway deletion in adult resting cardiac fibroblasts initiates a cell state transition with spontaneous and self-sustaining fibrosis. <i>Genes and Development</i> , 2019, 33, 1491-1505.	2.7	101
40	Deciphering Brain Complexity Using Single-cell Sequencing. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 344-366.	3.0	52
41	bayNorm: Bayesian gene expression recovery, imputation and normalization for single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2020, 36, 1174-1181.	1.8	79
42	EnImpute: imputing dropout events in single-cell RNA-sequencing data via ensemble learning. <i>Bioinformatics</i> , 2019, 35, 4827-4829.	1.8	29
43	Functional genomics in cancer immunotherapy: computational approaches for biomarker and drug discovery. <i>Molecular Systems Design and Engineering</i> , 2019, 4, 689-700.	1.7	3
44	Comprehensive Integration of Single-Cell Data. <i>Cell</i> , 2019, 177, 1888-1902.e21.	13.5	9,755
45	Geometric Sketching Compactly Summarizes the Single-Cell Transcriptomic Landscape. <i>Cell Systems</i> , 2019, 8, 483-493.e7.	2.9	95
46	Single-cell transcriptomics unveils gene regulatory network plasticity. <i>Genome Biology</i> , 2019, 20, 110.	3.8	170
47	Simulating multiple faceted variability in single cell RNA sequencing. <i>Nature Communications</i> , 2019, 10, 2611.	5.8	89
48	DECENT: differential expression with capture efficiency adjustment for single-cell RNA-seq data. <i>Bioinformatics</i> , 2019, 35, 5155-5162.	1.8	33
49	Single-Cell RNA-Seq Analysis of Retinal Development Identifies NFI Factors as Regulating Mitotic Exit and Late-Born Cell Specification. <i>Neuron</i> , 2019, 102, 1111-1126.e5.	3.8	343
50	Gene Regulatory Networks from Single Cell Data for Exploring Cell Fate Decisions. <i>Methods in Molecular Biology</i> , 2019, 1975, 211-238.	0.4	3
51	Genome-scale screens identify JNK/JUN signaling as a barrier for pluripotency exit and endoderm differentiation. <i>Nature Genetics</i> , 2019, 51, 999-1010.	9.4	90
52	SCRABBLE: single-cell RNA-seq imputation constrained by bulk RNA-seq data. <i>Genome Biology</i> , 2019, 20, 88.	3.8	88
53	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. <i>Cell Systems</i> , 2019, 8, 315-328.e8.	2.9	117
54	Targeting TMEM176B Enhances Antitumor Immunity and Augments the Efficacy of Immune Checkpoint Blockers by Unleashing Inflammasome Activation. <i>Cancer Cell</i> , 2019, 35, 767-781.e6.	7.7	91
55	scNPF: an integrative framework assisted by network propagation and network fusion for preprocessing of single-cell RNA-seq data. <i>BMC Genomics</i> , 2019, 20, 347.	1.2	11

#	ARTICLE	IF	CITATIONS
56	Natural Genetic Variation Reveals Key Features of Epigenetic and Transcriptional Memory in Virus-Specific CD8 ⁺ T Cells. <i>Immunity</i> , 2019, 50, 1202-1217.e7.	6.6	51
57	Drug resistance: origins, evolution and characterization of genomic clones and the tumor ecosystem to optimize precise individualized therapy. <i>Drug Discovery Today</i> , 2019, 24, 1281-1294.	3.2	25
58	Efficient integration of heterogeneous single-cell transcriptomes using Scanorama. <i>Nature Biotechnology</i> , 2019, 37, 685-691.	9.4	557
59	The emergent landscape of the mouse gut endoderm at single-cell resolution. <i>Nature</i> , 2019, 569, 361-367.	13.7	285
60	Network Medicine in Pathobiology. <i>American Journal of Pathology</i> , 2019, 189, 1311-1326.	1.9	55
61	Characterization of cell fate probabilities in single-cell data with Palantir. <i>Nature Biotechnology</i> , 2019, 37, 451-460.	9.4	393
62	Scalable analysis of cell-type composition from single-cell transcriptomics using deep recurrent learning. <i>Nature Methods</i> , 2019, 16, 311-314.	9.0	142
63	Negative Co-stimulation Constrains T Cell Differentiation by Imposing Boundaries on Possible Cell States. <i>Immunity</i> , 2019, 50, 1084-1098.e10.	6.6	75
64	Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 317.	1.1	611
65	Defining developmental diversification of diencephalon neurons through single-cell gene expression profiling. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	28
66	Clustering single-cell RNA-seq data with a model-based deep learning approach. <i>Nature Machine Intelligence</i> , 2019, 1, 191-198.	8.3	189
67	An Informative Approach to Single-Cell Sequencing Analysis. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1129, 81-96.	0.8	3
68	Modeling the Pathological Long-Range Regulatory Effects of Human Structural Variation with Patient-Specific hiPSCs. <i>Cell Stem Cell</i> , 2019, 24, 736-752.e12.	5.2	90
69	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	3.1	57
70	DoubletFinder: Doublet Detection in Single-Cell RNA Sequencing Data Using Artificial Nearest Neighbors. <i>Cell Systems</i> , 2019, 8, 329-337.e4.	2.9	1,648
71	NR4A transcription factors limit CAR T cell function in solid tumours. <i>Nature</i> , 2019, 567, 530-534.	13.7	519
72	Coarse Graining of Data via Inhomogeneous Diffusion Condensation. , 2019, 2019, 2624-2633.		9
73	RIA: a novel Regression-based Imputation Approach for single-cell RNA sequencing. , 2019, , .		4

#	ARTICLE	IF	CITATIONS
74	Dropout imputation and batch effect correction for single-cell RNA sequencing data. <i>Journal of Bio-X Research</i> , 2019, 2, 169-177.	0.3	2
75	Finding Archetypal Spaces Using Neural Networks. , 2019, , .		9
76	Novel dynamics of human mucociliary differentiation revealed by single-cell RNA sequencing of nasal epithelial cultures. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	208
77	scRNA-seq in medulloblastoma shows cellular heterogeneity and lineage expansion support resistance to SHH inhibitor therapy. <i>Nature Communications</i> , 2019, 10, 5829.	5.8	77
78	Using transfer learning from prior reference knowledge to improve the clustering of single-cell RNA-Seq data. <i>Scientific Reports</i> , 2019, 9, 20353.	1.6	23
79	Reconstruction of Cell-type-Specific Interactomes at Single-Cell Resolution. <i>Cell Systems</i> , 2019, 9, 559-568.e4.	2.9	51
80	Intra-lineage Plasticity and Functional Reprogramming Maintain Natural Killer Cell Repertoire Diversity. <i>Cell Reports</i> , 2019, 29, 2284-2294.e4.	2.9	33
81	Mapping lung cancer epithelial-mesenchymal transition states and trajectories with single-cell resolution. <i>Nature Communications</i> , 2019, 10, 5587.	5.8	162
82	MLL-AF9 initiates transformation from fast-proliferating myeloid progenitors. <i>Nature Communications</i> , 2019, 10, 5767.	5.8	41
83	Emerging deep learning methods for single-cell RNA-seq data analysis. <i>Quantitative Biology</i> , 2019, 7, 247-254.	0.3	25
84	Theory of cell fate. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1471.	6.6	19
85	Exploring single-cell data with deep multitasking neural networks. <i>Nature Methods</i> , 2019, 16, 1139-1145.	9.0	222
86	Visualizing structure and transitions in high-dimensional biological data. <i>Nature Biotechnology</i> , 2019, 37, 1482-1492.	9.4	597
87	Single-cell RNA-Seq of follicular lymphoma reveals malignant B-cell types and coexpression of T-cell immune checkpoints. <i>Blood</i> , 2019, 133, 1119-1129.	0.6	99
88	Single-Cell RNA-Seq of the Pancreatic Isletsâ€“a Promise Not yet Fulfilled?. <i>Cell Metabolism</i> , 2019, 29, 539-544.	7.2	98
89	A test metric for assessing single-cell RNA-seq batch correction. <i>Nature Methods</i> , 2019, 16, 43-49.	9.0	278
90	A complex auxiliary: IL-17/Th17 signaling during type 1 diabetes progression. <i>Molecular Immunology</i> , 2019, 105, 16-31.	1.0	14
91	High-performance medicine: the convergence of human and artificial intelligence. <i>Nature Medicine</i> , 2019, 25, 44-56.	15.2	2,938

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92	Single-Cell Applications of Next-Generation Sequencing. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a026898.	2.9	23
93	Challenges in unsupervised clustering of single-cell RNA-seq data. Nature Reviews Genetics, 2019, 20, 273-282.	7.7	780
94	A cluster robustness score for identifying cell subpopulations in single cell gene expression datasets from heterogeneous tissues and tumors. Bioinformatics, 2019, 35, 962-971.	1.8	12
95	Autocrine regulation of mesenchymal progenitor cell fates orchestrates tooth eruption. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 575-580.	3.3	91
96	Gene Regulatory Networks. Methods in Molecular Biology, 2019, , .	0.4	41
97	Network Inference from Single-Cell Transcriptomic Data. Methods in Molecular Biology, 2019, 1883, 235-249.	0.4	23
98	Hybrid epithelial/mesenchymal phenotypes promote metastasis and therapy resistance across carcinomas. , 2019, 194, 161-184.		244
99	Cancer Stem Cells and Epithelial-to-Mesenchymal Transition in Cancer Metastasis. Cold Spring Harbor Perspectives in Medicine, 2020, 10, a036905.	2.9	98
100	MCPyV Large T Antigen-Induced Atonal Homolog 1 Is a Lineage-Dependency Oncogene in Merkel Cell Carcinoma. Journal of Investigative Dermatology, 2020, 140, 56-65.e3.	0.3	35
101	Rho-mediated signaling promotes BRAF inhibitor resistance in de-differentiated melanoma cells. Oncogene, 2020, 39, 1466-1483.	2.6	40
102	Network control principles for identifying personalized driver genes in cancer. Briefings in Bioinformatics, 2020, 21, 1641-1662.	3.2	29
103	Rapid non-uniform adaptation to conformation-specific KRAS(G12C) inhibition. Nature, 2020, 577, 421-425.	13.7	321
104	Realistic in silico generation and augmentation of single-cell RNA-seq data using generative adversarial networks. Nature Communications, 2020, 11, 166.	5.8	118
105	Combined single-cell and spatial transcriptomics reveal the molecular, cellular and spatial bone marrow niche organization. Nature Cell Biology, 2020, 22, 38-48.	4.6	521
106	Immune profiling of human tumors identifies CD73 as a combinatorial target in glioblastoma. Nature Medicine, 2020, 26, 39-46.	15.2	236
107	Multipotent RAG1+ progenitors emerge directly from haemogenic endothelium in human pluripotent stem cell-derived haematopoietic organoids. Nature Cell Biology, 2020, 22, 60-73.	4.6	37
108	A systems-level framework for anti-epilepsy drug discovery. Neuropharmacology, 2020, 170, 107868.	2.0	15
109	Dissecting the human immune system with single cell RNA sequencing technology. Journal of Leukocyte Biology, 2020, 107, 613-623.	1.5	13

#	ARTICLE	IF	CITATIONS
110	Single-Cell Expression Variability Implies Cell Function. <i>Cells</i> , 2020, 9, 14.	1.8	27
111	Network Inference Analysis Identifies SETDB1 as a Key Regulator for Reverting Colorectal Cancer Cells into Differentiated Normal-Like Cells. <i>Molecular Cancer Research</i> , 2020, 18, 118-129.	1.5	23
112	Dimensionality reduction for single cell RNA sequencing data using constrained robust non-negative matrix factorization. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa064.	1.5	10
113	Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. <i>EMBO Journal</i> , 2020, 39, e104063.	3.5	224
114	Improved detection of tumor suppressor events in single-cell RNA-Seq data. <i>Npj Genomic Medicine</i> , 2020, 5, 43.	1.7	15
115	SIMPLEs: a single-cell RNA sequencing imputation strategy preserving gene modules and cell clusters variation. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa077.	1.5	6
116	scLRTD : A Novel Low Rank Tensor Decomposition Method for Imputing Missing Values in Single-Cell Multi-Omics Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1144-1153.	1.9	5
117	Organoids Model Transcriptional Hallmarks of Oncogenic KRAS Activation in Lung Epithelial Progenitor Cells. <i>Cell Stem Cell</i> , 2020, 27, 663-678.e8.	5.2	86
118	Elucidation of Biological Networks across Complex Diseases Using Single-Cell Omics. <i>Trends in Genetics</i> , 2020, 36, 951-966.	2.9	23
119	Model-based autoencoders for imputing discrete single-cell RNA-seq data. <i>Methods</i> , 2021, 192, 112-119.	1.9	10
120	Single-Cell Transcriptome Analysis of Colon Cancer Cell Response to 5-Fluorouracil-Induced DNA Damage. <i>Cell Reports</i> , 2020, 32, 108077.	2.9	40
121	SERGIO: A Single-Cell Expression Simulator Guided by Gene Regulatory Networks. <i>Cell Systems</i> , 2020, 11, 252-271.e11.	2.9	59
122	Sequencing dropout-and-batch effect normalization for single-cell mRNA profiles: a survey and comparative analysis. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	4
123	The Stress-Like Cancer Cell State Is a Consistent Component of Tumorigenesis. <i>Cell Systems</i> , 2020, 11, 536-546.e7.	2.9	65
124	An era of single-cell genomics consortia. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1409-1418.	3.2	12
125	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. <i>Nature</i> , 2020, 586, 769-775.	13.7	101
126	Leveraging Uncertainty in Machine Learning Accelerates Biological Discovery and Design. <i>Cell Systems</i> , 2020, 11, 461-477.e9.	2.9	92
127	Random Parametric Perturbations of Gene Regulatory Circuit Uncover State Transitions in Cell Cycle. <i>IScience</i> , 2020, 23, 101150.	1.9	12

#	ARTICLE	IF	CITATIONS
128	A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification. <i>Bioinformatics</i> , 2020, 36, i292-i299.	1.8	13
129	A Random Matrix Theory Approach to Denoise Single-Cell Data. <i>Patterns</i> , 2020, 1, 100035.	3.1	30
130	Cancer cells deploy lipocalin-2 to collect limiting iron in leptomeningeal metastasis. <i>Science</i> , 2020, 369, 276-282.	6.0	146
131	Integrating Deep Supervised, Self-Supervised and Unsupervised Learning for Single-Cell RNA-seq Clustering and Annotation. <i>Genes</i> , 2020, 11, 792.	1.0	23
132	DISC: a highly scalable and accurate inference of gene expression and structure for single-cell transcriptomes using semi-supervised deep learning. <i>Genome Biology</i> , 2020, 21, 170.	3.8	26
133	Macrophage subsets in atherosclerosis as defined by single-cell technologies. <i>Journal of Pathology</i> , 2020, 250, 705-714.	2.1	127
134	EC-PGMGR: Ensemble Clustering Based on Probability Graphical Model With Graph Regularization for Single-Cell RNA-seq Data. <i>Frontiers in Genetics</i> , 2020, 11, 572242.	1.1	4
135	Are dropout imputation methods for scRNA-seq effective for scHi-C data?. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
136	Liver Immune Profiling Reveals Pathogenesis and Therapeutics for Biliary Atresia. <i>Cell</i> , 2020, 183, 1867-1883.e26.	13.5	70
137	Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. <i>Cell Reports</i> , 2020, 33, 108448.	2.9	35
138	Ultra-fast scalable estimation of single-cell differentiation potency from scRNA-Seq data. <i>Bioinformatics</i> , 2021, 37, 1528-1534.	1.8	13
139	Comprehensive analysis of single-cell RNA sequencing data from healthy human marrow hematopoietic cells. <i>BMC Research Notes</i> , 2020, 13, 514.	0.6	5
140	SARS-CoV-2 receptor is co-expressed with elements of the kinin-kallikrein, renin-angiotensin and coagulation systems in alveolar cells. <i>Scientific Reports</i> , 2020, 10, 19522.	1.6	39
141	scTenifoldNet: A Machine Learning Workflow for Constructing and Comparing Transcriptome-wide Gene Regulatory Networks from Single-Cell Data. <i>Patterns</i> , 2020, 1, 100139.	3.1	25
142	Dissecting genetic determinants of variation in human immune responses. <i>Current Opinion in Immunology</i> , 2020, 65, 74-78.	2.4	3
143	Comparative Research of Different Dimension Reduction Methods Combined with RWR Network Smoothing in Single Cell RNA-seq Data. <i>IOP Conference Series: Earth and Environmental Science</i> , 2020, 495, 012043.	0.2	0
144	In Vivo Chimeric Alzheimer's Disease Modeling of Apolipoprotein E4 Toxicity in Human Neurons. <i>Cell Reports</i> , 2020, 32, 107962.	2.9	30
145	A molecular map of murine lymph node blood vascular endothelium at single cell resolution. <i>Nature Communications</i> , 2020, 11, 3798.	5.8	74

#	ARTICLE	IF	CITATIONS
146	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. <i>Nature Methods</i> , 2020, 17, 793-798.	9.0	134
147	Antibody-secreting cell destiny emerges during the initial stages of B-cell activation. <i>Nature Communications</i> , 2020, 11, 3989.	5.8	41
148	Patterns, Profiles, and Parsimony: Dissecting Transcriptional Signatures From Minimal Single-Cell RNA-Seq Output With SALSA. <i>Frontiers in Genetics</i> , 2020, 11, 511286.	1.1	1
149	Single-Cell Transcriptomics Reveals Early Emergence of Liver Parenchymal and Non-parenchymal Cell Lineages. <i>Cell</i> , 2020, 183, 702-716.e14.	13.5	52
150	Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimer's and Parkinson's diseases. <i>Nature Genetics</i> , 2020, 52, 1158-1168.	9.4	217
151	Multi-Omics Resolves a Sharp Disease-State Shift between Mild and Moderate COVID-19. <i>Cell</i> , 2020, 183, 1479-1495.e20.	13.5	449
152	Probing infectious disease by single-cell RNA sequencing: Progresses and perspectives. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2962-2971.	1.9	32
153	A review of computational strategies for denoising and imputation of single-cell transcriptomic data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	27
154	The era of big data: Genome-scale modelling meets machine learning. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3287-3300.	1.9	47
155	Single-cell RNA sequencing identifies shared differentiation paths of mouse thymic innate T cells. <i>Nature Communications</i> , 2020, 11, 4367.	5.8	56
156	Developing the novel bioinformatics algorithms to systematically investigate the connections among survival time, key genes and proteins for Glioblastoma multiforme. <i>BMC Bioinformatics</i> , 2020, 21, 383.	1.2	9
157	A novel single-cell based method for breast cancer prognosis. <i>PLoS Computational Biology</i> , 2020, 16, e1008133.	1.5	16
158	A systematic evaluation of single-cell RNA-sequencing imputation methods. <i>Genome Biology</i> , 2020, 21, 218.	3.8	188
159	Single-cell sequencing techniques from individual to multiomics analyses. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1419-1427.	3.2	136
160	Transcriptomic and clonal characterization of T cells in the human central nervous system. <i>Science Immunology</i> , 2020, 5, .	5.6	73
161	Diversification of reprogramming trajectories revealed by parallel single-cell transcriptome and chromatin accessibility sequencing. <i>Science Advances</i> , 2020, 6, .	4.7	37
162	High accuracy gene expression profiling of sorted cell subpopulations from breast cancer PDX model tissue. <i>PLoS ONE</i> , 2020, 15, e0238594.	1.1	1
163	Pinpointing Cell Identity in Time and Space. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 209.	1.6	15

#	ARTICLE	IF	CITATIONS
164	Immune-evasive human islet-like organoids ameliorate diabetes. <i>Nature</i> , 2020, 586, 606-611.	13.7	192
165	Harmonic Alignment. , 2020, 2020, 316-324.		9
166	Goals and approaches for each processing step for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	31
167	Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and A β Accumulation in Alzheimer's Disease. <i>Cell Reports</i> , 2020, 33, 108447.	2.9	26
168	scGMAI: a Gaussian mixture model for clustering single-cell RNA-Seq data based on deep autoencoder. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	26
169	Mouse embryonic stem cells self-organize into trunk-like structures with neural tube and somites. <i>Science</i> , 2020, 370, .	6.0	193
170	GCNG: graph convolutional networks for inferring gene interaction from spatial transcriptomics data. <i>Genome Biology</i> , 2020, 21, 300.	3.8	83
171	A Review of Integrative Imputation for Multi-Omics Datasets. <i>Frontiers in Genetics</i> , 2020, 11, 570255.	1.1	57
172	Single-Cell Profiling of Ebola Virus Disease In Vivo Reveals Viral and Host Dynamics. <i>Cell</i> , 2020, 183, 1383-1401.e19.	13.5	79
173	scAIDE: clustering of large-scale single-cell RNA-seq data reveals putative and rare cell types. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa082.	1.5	21
174	A rank-based marker selection method for high throughput scRNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 477.	1.2	29
175	Defining the Teratoma as a Model for Multi-lineage Human Development. <i>Cell</i> , 2020, 183, 1402-1419.e18.	13.5	32
176	A map of tumor-host interactions in glioma at single-cell resolution. <i>GigaScience</i> , 2020, 9, .	3.3	32
177	Mitochondria Define Intestinal Stem Cell Differentiation Downstream of a FOXO/Notch Axis. <i>Cell Metabolism</i> , 2020, 32, 889-900.e7.	7.2	90
178	Integrated single-cell and bulk gene expression and ATAC-seq reveals heterogeneity and early changes in pathways associated with resistance to cetuximab in HNSCC-sensitive cell lines. <i>British Journal of Cancer</i> , 2020, 123, 101-113.	2.9	38
179	Gene regulatory network reconstruction using single-cell RNA sequencing of barcoded genotypes in diverse environments. <i>ELife</i> , 2020, 9, .	2.8	116
180	A Single-Cell Transcriptional Roadmap of the Mouse and Human Lymph Node Lymphatic Vasculature. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 52.	1.1	97
181	TMPRSS2 and TMPRSS4 promote SARS-CoV-2 infection of human small intestinal enterocytes. <i>Science Immunology</i> , 2020, 5, .	5.6	811

#	ARTICLE	IF	CITATIONS
182	APEC: an accession-based method for single-cell chromatin accessibility analysis. <i>Genome Biology</i> , 2020, 21, 116.	3.8	12
183	Computational Methods for Single-Cell RNA Sequencing. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 339-364.	2.8	81
184	Sparsity-Penalized Stacked Denoising Autoencoders for Imputing Single-Cell RNA-seq Data. <i>Genes</i> , 2020, 11, 532.	1.0	8
185	Early precursors and molecular determinants of tissue-resident memory CD8 ⁺ T lymphocytes revealed by single-cell RNA sequencing. <i>Science Immunology</i> , 2020, 5, .	5.6	124
186	Quantitative single-cell interactomes in normal and virus-infected mouse lungs. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, .	1.2	13
187	An Erg-driven transcriptional program controls B cell lymphopoiesis. <i>Nature Communications</i> , 2020, 11, 3013.	5.8	29
188	Circulating immune cell phenotype dynamics reflect the strength of tumor-immune cell interactions in patients during immunotherapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16072-16082.	3.3	60
189	A scalable SCENIC workflow for single-cell gene regulatory network analysis. <i>Nature Protocols</i> , 2020, 15, 2247-2276.	5.5	553
190	A long noncoding RNA regulates inflammation resolution by mouse macrophages through fatty acid oxidation activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14365-14375.	3.3	39
191	A flexible network-based imputing-and-fusing approach towards the identification of cell types from single-cell RNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 240.	1.2	2
192	Sequencing of RNA in single cells reveals a distinct transcriptome signature of hematopoiesis in GATA2 deficiency. <i>Blood Advances</i> , 2020, 4, 2702-2716.	2.5	23
193	Network Diffusion Promotes the Integrative Analysis of Multiple Omics. <i>Frontiers in Genetics</i> , 2020, 11, 106.	1.1	21
194	Imputation of single-cell gene expression with an autoencoder neural network. <i>Quantitative Biology</i> , 2020, 8, 78-94.	0.3	40
195	Bayesian correlation is a robust gene similarity measure for single-cell RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa002.	1.5	17
196	Advanced Computational Intelligence in Healthcare-7. <i>Studies in Computational Intelligence</i> , 2020, , .	0.7	3
197	Dynamic Transcriptional Responses to Injury of Regenerative and Non-regenerative Cardiomyocytes Revealed by Single-Nucleus RNA Sequencing. <i>Developmental Cell</i> , 2020, 53, 102-116.e8.	3.1	95
198	Tools for the analysis of high-dimensional single-cell RNA sequencing data. <i>Nature Reviews Nephrology</i> , 2020, 16, 408-421.	4.1	80
199	Embracing the dropouts in single-cell RNA-seq analysis. <i>Nature Communications</i> , 2020, 11, 1169.	5.8	204

#	ARTICLE	IF	CITATIONS
200	Adult Human Glioblastomas Harbor Radial Glia-like Cells. <i>Stem Cell Reports</i> , 2020, 14, 338-350.	2.3	35
201	A dopamine-induced gene expression signature regulates neuronal function and cocaine response. <i>Science Advances</i> , 2020, 6, eaba4221.	4.7	114
202	scIGANs: single-cell RNA-seq imputation using generative adversarial networks. <i>Nucleic Acids Research</i> , 2020, 48, e85-e85.	6.5	93
203	Dual indexed library design enables compatibility of in-Drop single-cell RNA-sequencing with exAMP chemistry sequencing platforms. <i>BMC Genomics</i> , 2020, 21, 456.	1.2	22
204	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	3.8	742
205	scRMD: imputation for single cell RNA-seq data via robust matrix decomposition. <i>Bioinformatics</i> , 2020, 36, 3156-3161.	1.8	42
206	Cell-type-specific signaling networks in heterocellular organoids. <i>Nature Methods</i> , 2020, 17, 335-342.	9.0	75
207	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. <i>Bioinformatics</i> , 2020, 36, 3131-3138.	1.8	22
208	Crosstalk with lung epithelial cells regulates Sfrp2-mediated latency in breast cancer dissemination. <i>Nature Cell Biology</i> , 2020, 22, 289-296.	4.6	67
209	Tumour heterogeneity and the evolutionary trade-offs of cancer. <i>Nature Reviews Cancer</i> , 2020, 20, 247-257.	12.8	111
210	2DImpute: imputation in single-cell RNA-seq data from correlations in two dimensions. <i>Bioinformatics</i> , 2020, 36, 3588-3589.	1.8	13
211	Learning Pathway Dynamics from Single-Cell Proteomic Data: A Comparative Study. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 241-252.	1.1	3
212	Regenerative lineages and immune-mediated pruning in lung cancer metastasis. <i>Nature Medicine</i> , 2020, 26, 259-269.	15.2	274
213	CLEAR: coverage-based limiting-cell experiment analysis for RNA-seq. <i>Journal of Translational Medicine</i> , 2020, 18, 63.	1.8	11
214	Droplet scRNA-seq is not zero-inflated. <i>Nature Biotechnology</i> , 2020, 38, 147-150.	9.4	248
215	Uncovering axes of variation among single-cell cancer specimens. <i>Nature Methods</i> , 2020, 17, 302-310.	9.0	39
216	Microglia response following acute demyelination is heterogeneous and limits infiltrating macrophage dispersion. <i>Science Advances</i> , 2020, 6, eaay6324.	4.7	130
217	Single cell and genetic analyses reveal conserved populations and signaling mechanisms of gastrointestinal stromal niches. <i>Nature Communications</i> , 2020, 11, 334.	5.8	73

#	ARTICLE	IF	CITATIONS
218	Recurrent pregnancy loss is associated with a pro-senescent decidual response during the peri-implantation window. <i>Communications Biology</i> , 2020, 3, 37.	2.0	158
219	Benchmarking principal component analysis for large-scale single-cell RNA-sequencing. <i>Genome Biology</i> , 2020, 21, 9.	3.8	71
220	L1CAM defines the regenerative origin of metastasis-initiating cells in colorectal cancer. <i>Nature Cancer</i> , 2020, 1, 28-45.	5.7	137
221	netNMF-sc: leveraging gene-gene interactions for imputation and dimensionality reduction in single-cell expression analysis. <i>Genome Research</i> , 2020, 30, 195-204.	2.4	61
222	PRIME: a probabilistic imputation method to reduce dropout effects in single-cell RNA sequencing. <i>Bioinformatics</i> , 2020, 36, 4021-4029.	1.8	17
223	CD4+ teff cell heterogeneity: the perspective from single-cell transcriptomics. <i>Current Opinion in Immunology</i> , 2020, 63, 61-67.	2.4	18
224	Single Cell Analysis in Vascular Biology. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 42.	1.1	51
225	Single Cell RNA Sequencing in Atherosclerosis Research. <i>Circulation Research</i> , 2020, 126, 1112-1126.	2.0	84
226	Scedar: A scalable Python package for single-cell RNA-seq exploratory data analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1007794.	1.5	9
227	Profiling Cell Signaling Networks at Single-cell Resolution. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 744-756.	2.5	39
228	Toward Community-Driven Big Open Brain Science: Open Big Data and Tools for Structure, Function, and Genetics. <i>Annual Review of Neuroscience</i> , 2020, 43, 441-464.	5.0	12
229	EMT Factors and Metabolic Pathways in Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 499.	1.3	205
230	Endocrine-Exocrine Signaling Drives Obesity-Associated Pancreatic Ductal Adenocarcinoma. <i>Cell</i> , 2020, 181, 832-847.e18.	13.5	77
231	Network-Based Single-Cell RNA-Seq Data Imputation Enhances Cell Type Identification. <i>Genes</i> , 2020, 11, 377.	1.0	13
232	SCCLRR: A Robust Computational Method for Accurate Clustering Single Cell RNA-Seq Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 247-256.	3.9	17
233	Evaluating genetic causes of azoospermia: What can we learn from a complex cellular structure and single-cell transcriptomics of the human testis?. <i>Human Genetics</i> , 2021, 140, 183-201.	1.8	29
234	Imputing single-cell RNA-seq data by considering cell heterogeneity and prior expression of dropouts. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 29-40.	1.5	21
235	The future of cerebral organoids in drug discovery. <i>Seminars in Cell and Developmental Biology</i> , 2021, 111, 67-73.	2.3	15

#	ARTICLE	IF	CITATIONS
236	A comprehensive survey of regulatory network inference methods using single cell RNA sequencing data. Briefings in Bioinformatics, 2021, 22, .	3.2	92
237	mTORC1 hyperactivation in lymphangioleiomyomatosis leads to <i>ACE2</i> upregulation in type II pneumocytes: implications for COVID-19. European Respiratory Journal, 2021, 57, 2002737.	3.1	11
238	Predictive modeling of single-cell DNA methylome data enhances integration with transcriptome data. Genome Research, 2021, 31, 101-109.	2.4	12
239	Macrophage expression and prognostic significance of the long pentraxin PTX3 in COVID-19. Nature Immunology, 2021, 22, 19-24.	7.0	101
240	TENET: gene network reconstruction using transfer entropy reveals key regulatory factors from single cell transcriptomic data. Nucleic Acids Research, 2021, 49, e1-e1.	6.5	26
241	Senescence Reprogramming by TIMP1 Deficiency Promotes Prostate Cancer Metastasis. Cancer Cell, 2021, 39, 68-82.e9.	7.7	66
242	Tutorial: guidelines for the computational analysis of single-cell RNA sequencing data. Nature Protocols, 2021, 16, 1-9.	5.5	169
243	Entropy subspace separation-based clustering for noise reduction (ENCORE) of scRNA-seq data. Nucleic Acids Research, 2021, 49, e18-e18.	6.5	10
244	A primer on single-cell genomics in myeloid biology. Current Opinion in Hematology, 2021, 28, 11-17.	1.2	0
245	Benchmarking Computational Doublet-Detection Methods for Single-Cell RNA Sequencing Data. Cell Systems, 2021, 12, 176-194.e6.	2.9	99
246	Holistic characterization of single-hepatocyte transcriptome responses to high-fat diet. American Journal of Physiology - Endocrinology and Metabolism, 2021, 320, E244-E258.	1.8	17
248	The winning methods for predicting cellular position in the DREAM single-cell transcriptomics challenge. Briefings in Bioinformatics, 2021, 22, .	3.2	4
249	Bfimpute: A Bayesian Factorization Method to Recover Single-Cell Rna Sequencing Data. SSRN Electronic Journal, 0, , .	0.4	0
250	<i>Nebulosa</i> recovers single-cell gene expression signals by kernel density estimation. Bioinformatics, 2021, 37, 2485-2487.	1.8	133
251	Single-Cell RNA Sequencing Data Imputation Using Deep Neural Network. Advances in Intelligent Systems and Computing, 2021, , 403-410.	0.5	1
252	Loss of Claudin-3 Impairs Hepatic Metabolism, Biliary Barrier Function, and Cell Proliferation in the Murine Liver. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 745-767.	2.3	5
253	JOINT for large-scale single-cell RNA-sequencing analysis via soft-clustering and parallel computing. BMC Genomics, 2021, 22, 47.	1.2	3
254	Machine Learning and Deep Learning in Genetics and Genomics. , 2021, , 163-181.		3

#	ARTICLE	IF	CITATIONS
255	Single-Cell Sequencing of Brain Cell Transcriptomes and Epigenomes. <i>Neuron</i> , 2021, 109, 11-26.	3.8	135
257	Analysis of microRNA Regulation in Single Cells. <i>Methods in Molecular Biology</i> , 2021, 2243, 339-354.	0.4	3
258	Inference of Networks from Large Datasets. , 2021, , 17-25.		0
261	EnTSSR: A Weighted Ensemble Learning Method to Impute Single-Cell RNA Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2781-2787.	1.9	5
264	Gut CD4+ T cell phenotypes are a continuum molded by microbes, not by TH archetypes. <i>Nature Immunology</i> , 2021, 22, 216-228.	7.0	116
265	Integrated spatial genomics reveals global architecture of single nuclei. <i>Nature</i> , 2021, 590, 344-350.	13.7	228
267	Single-Cell RNA Sequencing Analysis: A Step-by-Step Overview. <i>Methods in Molecular Biology</i> , 2021, 2284, 343-365.	0.4	65
269	Single-Cell Analysis of Blood-Brain Barrier Response to Pericyte Loss. <i>Circulation Research</i> , 2021, 128, e46-e62.	2.0	98
270	Fully defined human pluripotent stem cell-derived microglia and tri-culture system model C3 production in Alzheimer's disease. <i>Nature Neuroscience</i> , 2021, 24, 343-354.	7.1	118
273	DeePaN: deep patient graph convolutional network integrating clinico-genomic evidence to stratify lung cancers for immunotherapy. <i>Npj Digital Medicine</i> , 2021, 4, 14.	5.7	23
274	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 282-291.	3.0	21
275	Clustering Single-Cell RNA-Seq Data with Regularized Gaussian Graphical Model. <i>Genes</i> , 2021, 12, 311.	1.0	9
276	Potential applications of deep learning in single-cell RNA sequencing analysis for cell therapy and regenerative medicine. <i>Stem Cells</i> , 2021, 39, 511-521.	1.4	16
277	Determinants, mechanisms, and functional outcomes of myeloid cell diversity in cancer. <i>Immunological Reviews</i> , 2021, 300, 220-236.	2.8	5
279	Quantifying the effect of experimental perturbations at single-cell resolution. <i>Nature Biotechnology</i> , 2021, 39, 619-629.	9.4	98
280	Network Modeling in Biology: Statistical Methods for Gene and Brain Networks. <i>Statistical Science</i> , 2021, 36, 89-108.	1.6	6
282	c-CSN: Single-cell RNA Sequencing Data Analysis by Conditional Cell-specific Network. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 319-329.	3.0	24
284	Cl1 Defines a Subset of Fibro-adipogenic Progenitors that Promote Skeletal Muscle Regeneration With Less Fat Accumulation. <i>Journal of Bone and Mineral Research</i> , 2020, 36, 1159-1173.	3.1	20

#	ARTICLE	IF	CITATIONS
286	Landscapes of cellular phenotypic diversity in breast cancer xenografts and their impact on drug response. <i>Nature Communications</i> , 2021, 12, 1998.	5.8	37
288	Single-cell RNA-seq dissects the intratumoral heterogeneity of triple-negative breast cancer based on gene regulatory networks. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 23, 682-690.	2.3	45
289	scGNN is a novel graph neural network framework for single-cell RNA-Seq analyses. <i>Nature Communications</i> , 2021, 12, 1882.	5.8	139
290	Noise regularization removes correlation artifacts in single-cell RNA-seq data preprocessing. <i>Patterns</i> , 2021, 2, 100211.	3.1	9
291	Cardiac macrophages prevent sudden death during heart stress. <i>Nature Communications</i> , 2021, 12, 1910.	5.8	41
292	A Regression Modeling Approach to Structured Shrinkage Estimation. <i>Journal of the American Statistical Association</i> , 0, , 1-11.	1.8	0
294	Beyond linearity, stability, and equilibrium: The edm package for empirical dynamic modeling and convergent cross-mapping in Stata. <i>The Stata Journal</i> , 2021, 21, 220-258.	0.9	4
296	Cellular plasticity balances the metabolic and proliferation dynamics of a regenerating liver. <i>Genome Research</i> , 2021, 31, 576-591.	2.4	53
297	Revealing lineage-related signals in single-cell gene expression using random matrix theory. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	8
298	Appyters: Turning Jupyter Notebooks into data-driven web apps. <i>Patterns</i> , 2021, 2, 100213.	3.1	58
303	DTFLOW: Inference and Visualization of Single-cell Pseudotime Trajectory Using Diffusion Propagation. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 306-318.	3.0	6
304	A hitchhiker's guide to single-cell transcriptomics and data analysis pipelines. <i>Genomics</i> , 2021, 113, 606-619.	1.3	44
306	WEDGE: imputation of gene expression values from single-cell RNA-seq datasets using biased matrix decomposition. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	17
307	The molecular landscape of neural differentiation in the developing <i>Drosophila</i> brain revealed by targeted scRNA-seq and multi-informatic analysis. <i>Cell Reports</i> , 2021, 35, 109039.	2.9	21
311	Bayesian inference of gene expression states from single-cell RNA-seq data. <i>Nature Biotechnology</i> , 2021, 39, 1008-1016.	9.4	50
312	Genetic Defects in DNAH2 Underlie Male Infertility With Multiple Morphological Abnormalities of the Sperm Flagella in Humans and Mice. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 662903.	1.8	22
313	Critical downstream analysis steps for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	33
319	Correlation AnalyzerR: functional predictions from gene co-expression correlations. <i>BMC Bioinformatics</i> , 2021, 22, 206.	1.2	46

#	ARTICLE	IF	CITATIONS
320	Low-N protein engineering with data-efficient deep learning. <i>Nature Methods</i> , 2021, 18, 389-396.	9.0	212
322	Stabilized epithelial phenotype of cancer cells in primary tumors leads to increased colonization of liver metastasis in pancreatic cancer. <i>Cell Reports</i> , 2021, 35, 108990.	2.9	49
323	<scp>SAREV</scp>: A review on statistical analytics of single-cell RNA sequencing data. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2022, 14, e1558.	2.1	2
324	A cis-regulatory atlas in maize at single-cell resolution. <i>Cell</i> , 2021, 184, 3041-3055.e21.	13.5	176
325	Anti-bias training for (sc)RNA-seq: experimental and computational approaches to improve precision. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
326	Cancer drug resistance induced by EMT: A novel therapeutic strategies. <i>Archives of Toxicology</i> , 2021, 95, 2279-2297.	1.9	92
327	Single-cell RNA sequencing of blood antigen-presenting cells in severe COVID-19 reveals multi-process defects in antiviral immunity. <i>Nature Cell Biology</i> , 2021, 23, 538-551.	4.6	114
328	Coupled analysis of transcriptome and BCR mutations reveals role of OXPHOS in affinity maturation. <i>Nature Immunology</i> , 2021, 22, 904-913.	7.0	62
329	scGRNom: a computational pipeline of integrative multi-omics analyses for predicting cell-type disease genes and regulatory networks. <i>Genome Medicine</i> , 2021, 13, 95.	3.6	21
330	Divergent clonal differentiation trajectories establish CD8+ memory T cell heterogeneity during acute viral infections in humans. <i>Cell Reports</i> , 2021, 35, 109174.	2.9	9
331	Imputing single-cell RNA-seq data by combining graph convolution and autoencoder neural networks. <i>IScience</i> , 2021, 24, 102393.	1.9	50
332	Phenotypic plasticity underlies local invasion and distant metastasis in colon cancer. <i>ELife</i> , 2021, 10, .	2.8	38
333	Big data analytics in single-cell transcriptomics: Five grand opportunities. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021, 11, e1414.	4.6	1
334	Machine Intelligence in Single-Cell Data Analysis: Advances and New Challenges. <i>Frontiers in Genetics</i> , 2021, 12, 655536.	1.1	33
335	G2S3: A gene graph-based imputation method for single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1009029.	1.5	6
336	Understanding the Adult Mammalian Heart at Single-Cell RNA-Seq Resolution. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 645276.	1.8	11
338	Multiomic Big Data Analysis Challenges: Increasing Confidence in the Interpretation of Artificial Intelligence Assessments. <i>Analytical Chemistry</i> , 2021, 93, 7763-7773.	3.2	18
339	Neuronal ApoE upregulates MHC-I expression to drive selective neurodegeneration in Alzheimer's disease. <i>Nature Neuroscience</i> , 2021, 24, 786-798.	7.1	91

#	ARTICLE	IF	CITATIONS
342	Integrated analysis of multimodal single-cell data. <i>Cell</i> , 2021, 184, 3573-3587.e29.	13.5	5,912
343	Epithelialâ€Mesenchymal Transition Associated with Head and Neck Squamous Cell Carcinomas: A Review. <i>Cancers</i> , 2021, 13, 3027.	1.7	18
344	Toward a Liver Cell Atlas: Understanding Liver Biology in Health and Disease at Single-Cell Resolution. <i>Seminars in Liver Disease</i> , 2021, 41, 321-330.	1.8	7
345	Consensus clustering of single-cell RNA-seq data by enhancing network affinity. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	24
347	Multi-Omics Approaches in Immunological Research. <i>Frontiers in Immunology</i> , 2021, 12, 668045.	2.2	22
350	SDImpute: A statistical block imputation method based on cell-level and gene-level information for dropouts in single-cell RNA-seq data. <i>PLoS Computational Biology</i> , 2021, 17, e1009118.	1.5	8
354	Medulloblastoma uses GABA transaminase to survive in the cerebrospinal fluid microenvironment and promote leptomeningeal dissemination. <i>Cell Reports</i> , 2021, 35, 109302.	2.9	19
355	Mammary gland development from a single cell â€omics view. <i>Seminars in Cell and Developmental Biology</i> , 2021, 114, 171-185.	2.3	18
356	mbImpute: an accurate and robust imputation method for microbiome data. <i>Genome Biology</i> , 2021, 22, 192.	3.8	23
357	A unified atlas of CD8 Tâ€cell dysfunctional states in cancer and infection. <i>Molecular Cell</i> , 2021, 81, 2477-2493.e10.	4.5	57
358	Single-Cell TCR and Transcriptome Analysis: An Indispensable Tool for Studying T-Cell Biology and Cancer Immunotherapy. <i>Frontiers in Immunology</i> , 2021, 12, 689091.	2.2	16
359	Computational systemsâ€biology approaches for modeling gene networks driving epithelialâ€mesenchymal transitions. <i>Computational and Systems Oncology</i> , 2021, 1, e1021.	1.1	12
360	COTAN: scRNA-seq data analysis based on gene co-expression. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab072.	1.5	11
364	Methylation of dual-specificity phosphatase 4 controls cell differentiation. <i>Cell Reports</i> , 2021, 36, 109421.	2.9	17
365	Profiling SARS-CoV-2 HLA-I peptidome reveals Tâ€cell epitopes from out-of-frame ORFs. <i>Cell</i> , 2021, 184, 3962-3980.e17.	13.5	98
366	Partial EMT in head and neck cancer biology: a spectrum instead of a switch. <i>Oncogene</i> , 2021, 40, 5049-5065.	2.6	56
367	Computing the Riemannian curvature of image patch and single-cell RNA sequencing data manifolds using extrinsic differential geometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	4
368	Metabolomic signatures in elite cyclists: differential characterization of a seeming normal endocrine status regarding three serum hormones. <i>Metabolomics</i> , 2021, 17, 67.	1.4	2

#	ARTICLE	IF	CITATIONS
369	SAILER: scalable and accurate invariant representation learning for single-cell ATAC-seq processing and integration. <i>Bioinformatics</i> , 2021, 37, i317-i326.	1.8	9
370	Mechanism-Centric Approaches for Biomarker Detection and Precision Therapeutics in Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 687813.	1.1	10
372	Regulatory T cells function in established systemic inflammation and reverse fatal autoimmunity. <i>Nature Immunology</i> , 2021, 22, 1163-1174.	7.0	33
374	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. <i>Cell</i> , 2021, 184, 4168-4185.e21.	13.5	203
375	Diffusion enables integration of heterogeneous data and user-driven learning in a desktop knowledge-base. <i>PLoS Computational Biology</i> , 2021, 17, e1009283.	1.5	4
376	Current Insights and Advancements in Head and Neck Cancer: Emerging Biomarkers and Therapeutics with Cues from Single Cell and 3D Model Omics Profiling. <i>Frontiers in Oncology</i> , 2021, 11, 676948.	1.3	5
377	DeepDRIM: a deep neural network to reconstruct cell-type-specific gene regulatory network using single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	28
378	Inhibition of WHSC1 Allows for Reprogramming of the Immune Compartment in Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8742.	1.8	6
379	FRMC: a fast and robust method for the imputation of scRNA-seq data. <i>RNA Biology</i> , 2021, , 1-10.	1.5	1
381	Single-cell lineage tracing of metastatic cancer reveals selection of hybrid EMT states. <i>Cancer Cell</i> , 2021, 39, 1150-1162.e9.	7.7	160
382	<i>DIAPH1</i> Variants in Non-“East Asian Patients With Sporadic Moyamoya Disease. <i>JAMA Neurology</i> , 2021, 78, 993.	4.5	33
383	AdImpute: An Imputation Method for Single-Cell RNA-Seq Data Based on Semi-Supervised Autoencoders. <i>Frontiers in Genetics</i> , 2021, 12, 739677.	1.1	7
384	Systems Analysis Reveals Ageing-Related Perturbations in Retinoids and Sex Hormones in Alzheimer’s and Parkinson’s Diseases. <i>Biomedicines</i> , 2021, 9, 1310.	1.4	8
385	Loss of polycomb repressive complex 1 activity and chromosomal instability drive uveal melanoma progression. <i>Nature Communications</i> , 2021, 12, 5402.	5.8	34
386	Ensemble Estimation of Generalized Mutual Information With Applications to Genomics. <i>IEEE Transactions on Information Theory</i> , 2021, 67, 5963-5996.	1.5	1
387	<i>HLF</i> expression defines the human hematopoietic stem cell state. <i>Blood</i> , 2021, 138, 2642-2654.	0.6	31
388	Generalized and scalable trajectory inference in single-cell omics data with VIA. <i>Nature Communications</i> , 2021, 12, 5528.	5.8	36
391	Single-cell analysis of prostaglandin E2-induced human decidual cell in vitro differentiation: a minimal ancestral decidual signal. <i>Biology of Reproduction</i> , 2022, 106, 155-172.	1.2	23

#	ARTICLE	IF	CITATIONS
392	EinImpute: a local and gene-based approach to imputation of dropout events in ScRNA-seq data. <i>Journal of Ambient Intelligence and Humanized Computing</i> , 2023, 14, 3225-3237.	3.3	2
393	A comparison of deep learning-based pre-processing and clustering approaches for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	14
394	Complement factor C1q mediates sleep spindle loss and epileptic spikes after mild brain injury. <i>Science</i> , 2021, 373, eabj2685.	6.0	55
395	High-throughput single-cell RNA-seq data imputation and characterization with surrogate-assisted automated deep learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
397	A single-cell tumor immune atlas for precision oncology. <i>Genome Research</i> , 2021, 31, 1913-1926.	2.4	87
398	Evaluation of some aspects in supervised cell type identification for single-cell RNA-seq: classifier, feature selection, and reference construction. <i>Genome Biology</i> , 2021, 22, 264.	3.8	21
399	Integrated analysis of plasma and single immune cells uncovers metabolic changes in individuals with COVID-19. <i>Nature Biotechnology</i> , 2022, 40, 110-120.	9.4	81
400	Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. <i>Cell</i> , 2021, 184, 5053-5069.e23.	13.5	209
401	Immune checkpoint blockade sensitivity and progression-free survival associates with baseline CD8 ⁺ T cell clone size and cytotoxicity. <i>Science Immunology</i> , 2021, 6, eabj8825.	5.6	41
402	The ETS transcription factor ERF controls the exit from the naïve pluripotent state in a MAPK-dependent manner. <i>Science Advances</i> , 2021, 7, eabg8306.	4.7	6
403	A reservoir of stem-like CD8 ⁺ T cells in the tumor-draining lymph node preserves the ongoing antitumor immune response. <i>Science Immunology</i> , 2021, 6, eabg7836.	5.6	123
404	Combinatorial therapy in tumor microenvironment: Where do we stand?. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021, 1876, 188585.	3.3	48
405	Machine learning for profile prediction in genomics. <i>Current Opinion in Chemical Biology</i> , 2021, 65, 35-41.	2.8	11
406	An MRI radiomics approach to predict survival and tumour-infiltrating macrophages in gliomas. <i>Brain</i> , 2022, 145, 1151-1161.	3.7	75
407	Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. <i>PLoS Computational Biology</i> , 2021, 17, e1008569.	1.5	19
408	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. <i>Nature Medicine</i> , 2021, 27, 141-151.	15.2	134
410	HOMC: A Hierarchical Clustering Algorithm Based on Optimal Low Rank Matrix Completion for Single Cell Analysis. <i>Lecture Notes in Computer Science</i> , 2021, , 66-76.	1.0	0
411	Elucidating the cellular dynamics of the brain with single-cell RNA sequencing. <i>RNA Biology</i> , 2021, 18, 1063-1084.	1.5	14

#	ARTICLE	IF	CITATIONS
412	Ancestral developmental potentials in early bony fish contributed to vertebrate water-to-land transition. <i>Zoological Research</i> , 2021, 42, 135-137.	0.9	5
413	Machine Learning Approaches on High Throughput NGS Data to Unveil Mechanisms of Function in Biology and Disease. <i>Cancer Genomics and Proteomics</i> , 2021, 18, 605-626.	1.0	11
414	Are dropout imputation methods for scRNA-seq effective for scATAC-seq data?. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
415	Statistical and Bioinformatics Analysis of Data from Bulk and Single-Cell RNA Sequencing Experiments. <i>Methods in Molecular Biology</i> , 2021, 2194, 143-175.	0.4	12
416	Joint learning of multiple gene networks from single-cell gene expression data. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2583-2595.	1.9	10
417	Heterogenous Populations of Tissue-Resident CD8+ T Cells Are Generated in Response to Infection and Malignancy. <i>Immunity</i> , 2020, 52, 808-824.e7.	6.6	149
418	Single-Cell RNA Sequencing of Tumor-Infiltrating NK Cells Reveals that Inhibition of Transcription Factor HIF-1 α Unleashes NK Cell Activity. <i>Immunity</i> , 2020, 52, 1075-1087.e8.	6.6	167
505	Accurately Clustering Single-cell RNA-seq data by Capturing Structural Relations between Cells through Graph Convolutional Network. , 2020, , .		26
506	Extendable and invertible manifold learning with geometry regularized autoencoders. , 2020, , .		8
507	A Computational Systems Biology Approach Identifies SLUG as a Mediator of Partial Epithelial-Mesenchymal Transition (EMT). <i>Cells Tissues Organs</i> , 2022, 211, 689-702.	1.3	36
508	Single-cell transcriptomics of alloreactive CD4+ T cells over time reveals divergent fates during gut graft-versus-host disease. <i>JCI Insight</i> , 2020, 5, .	2.3	12
509	Lack of Flvcr2 impairs brain angiogenesis without affecting the blood-brain barrier. <i>Journal of Clinical Investigation</i> , 2020, 130, 4055-4068.	3.9	11
510	Comprehensive network modeling from single cell RNA sequencing of human and mouse reveals well conserved transcription regulation of hematopoiesis. <i>BMC Genomics</i> , 2020, 21, 849.	1.2	9
511	Data Denoising and Post-Denoising Corrections in Single Cell RNA Sequencing. <i>Statistical Science</i> , 2020, 35, .	1.6	6
512	scClustViz “ Single-cell RNAseq cluster assessment and visualization. <i>F1000Research</i> , 2018, 7, 1522.	0.8	32
513	scClustViz “ Single-cell RNAseq cluster assessment and visualization. <i>F1000Research</i> , 2018, 7, 1522.	0.8	28
514	False signals induced by single-cell imputation. <i>F1000Research</i> , 2018, 7, 1740.	0.8	110
515	False signals induced by single-cell imputation. <i>F1000Research</i> , 2018, 7, 1740.	0.8	116

#	ARTICLE	IF	CITATIONS
516	Dissecting Cellular Heterogeneity Using Single-Cell RNA Sequencing. <i>Molecules and Cells</i> , 2019, 42, 189-199.	1.0	45
517	Phosphoproteomics identifies microglial Siglec ⁺ inflammatory response during neurodegeneration. <i>Molecular Systems Biology</i> , 2020, 16, e9819.	3.2	20
518	Artificial Intelligent in Healthcare. <i>Indonesian Biomedical Journal</i> , 2019, 11, 125-35.	0.2	4
519	Reconstructing gene regulatory networks in single-cell transcriptomic data analysis. <i>Zoological Research</i> , 2020, 41, 599-604.	0.9	8
520	Cancer systems immunology. <i>ELife</i> , 2020, 9, .	2.8	14
521	Diverse homeostatic and immunomodulatory roles of immune cells in the developing mouse lung at single cell resolution. <i>ELife</i> , 2020, 9, .	2.8	36
522	Matrix factorization for biomedical link prediction and scRNA-seq data imputation: an empirical survey. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	12
523	Deep learning-based advances and applications for single-cell RNA-sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	19
524	Alignment of single-cell trajectories by tuMap enables high-resolution quantitative comparison of cancer samples. <i>Cell Systems</i> , 2021, , .	2.9	3
525	An atlas of gene regulatory elements in adult mouse cerebrum. <i>Nature</i> , 2021, 598, 129-136.	13.7	95
526	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
527	Signatures of plasticity, metastasis, and immunosuppression in an atlas of human small cell lung cancer. <i>Cancer Cell</i> , 2021, 39, 1479-1496.e18.	7.7	155
529	Accurate Single-Cell Clustering through Ensemble Similarity Learning. <i>Genes</i> , 2021, 12, 1670.	1.0	0
530	Building the mega single-cell transcriptome ocular meta-atlas. <i>GigaScience</i> , 2021, 10, .	3.3	24
531	Single-cell epigenomics reveals mechanisms of human cortical development. <i>Nature</i> , 2021, 598, 205-213.	13.7	154
532	Experimental and real-world evidence supporting the computational repurposing of bumetanide for APOE4-related Alzheimer's disease. <i>Nature Aging</i> , 2021, 1, 932-947.	5.3	58
533	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. <i>Science Immunology</i> , 2021, 6, eabh3768.	5.6	19
537	Automated CUT&Tag profiling of chromatin heterogeneity in mixed-lineage leukemia. <i>Nature Genetics</i> , 2021, 53, 1586-1596.	9.4	42

#	ARTICLE	IF	CITATIONS
560	Paths and pathways that generate cell-type heterogeneity and developmental progression in hematopoiesis. <i>ELife</i> , 2021, 10, .	2.8	24
561	A Graph Feature Auto-Encoder for the prediction of unobserved node features on biological networks. <i>BMC Bioinformatics</i> , 2021, 22, 525.	1.2	8
562	Improving gene network inference with graph wavelets and making insights about ageing-associated regulatory changes in lungs. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
566	Recent Machine Learning Approaches for Single-Cell RNA-seq Data Analysis. <i>Studies in Computational Intelligence</i> , 2020, , 65-79.	0.7	3
576	Single-cell normalization and association testing unifying CRISPR screen and gene co-expression analyses with Normalizr. <i>Nature Communications</i> , 2021, 12, 6395.	5.8	13
577	Chromatin-accessibility estimation from single-cell ATAC-seq data with scOpen. <i>Nature Communications</i> , 2021, 12, 6386.	5.8	57
583	An Overview of Algorithms and Associated Applications for Single Cell RNA-Seq Data Imputation. <i>Current Genomics</i> , 2021, 22, 319-327.	0.7	5
588	FITs: forest of imputation trees for recovering true signals in single-cell open chromatin profiles. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa091.	1.5	2
590	Imputation in Scrna-seq Data Using Supervised Deep Generative Networks. , 2021, , .		0
591	Multimodal Data Visualization and Denoising with Integrated Diffusion. , 2021, 2021, .		15
592	Optimizing network propagation for multi-omics data integration. <i>PLoS Computational Biology</i> , 2021, 17, e1009161.	1.5	7
593	Self-organization of human dorsal-ventral forebrain structures by light induced SHH. <i>Nature Communications</i> , 2021, 12, 6768.	5.8	17
595	Single-Cell Genomics: Enabling the Functional Elucidation of Infectious Diseases in Multi-Cell Genomes. <i>Pathogens</i> , 2021, 10, 1467.	1.2	1
596	Single-cell proteo-genomic reference maps of the hematopoietic system enable the purification and massive profiling of precisely defined cell states. <i>Nature Immunology</i> , 2021, 22, 1577-1589.	7.0	76
597	A deep learning method for recovering missing signals in transcriptome-wide RNA structure profiles from probing experiments. <i>Nature Machine Intelligence</i> , 2021, 3, 995-1006.	8.3	2
598	Cell type identification from single-cell transcriptomes in melanoma. <i>BMC Medical Genomics</i> , 2021, 14, 263.	0.7	0
600	ScLRTC: imputation for single-cell RNA-seq data via low-rank tensor completion. <i>BMC Genomics</i> , 2021, 22, 860.	1.2	6
601	Single-cell transcriptomics reveals opposing roles of Shp2 in Myc-driven liver tumor cells and microenvironment. <i>Cell Reports</i> , 2021, 37, 109974.	2.9	26

#	ARTICLE	IF	CITATIONS
602	A Deep-Learning Pipeline for TSS Coverage Imputation From Shallow Cell-Free DNA Sequencing. <i>Frontiers in Medicine</i> , 2021, 8, 684238.	1.2	0
603	Dynamic prostate cancer transcriptome analysis delineates the trajectory to disease progression. <i>Nature Communications</i> , 2021, 12, 7033.	5.8	27
605	On the relation between input and output distributions of scRNA-seq experiments. <i>Bioinformatics</i> , 2022, 38, 1336-1343.	1.8	1
606	scCDG: A Method based on DAE and GCN for scRNA-seq data Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	16
607	Fast Computational Recovery of Missing Features for Large-scale Biological Data. <i>Springer Theses</i> , 2021, , 13-40.	0.0	0
608	A novel graph-based k-partitioning approach improves the detection of gene-gene correlations by single-cell RNA sequencing. <i>BMC Genomics</i> , 2022, 23, 35.	1.2	5
609	Engagement of the costimulatory molecule ICOS in tissues promotes establishment of CD8+ tissue-resident memory T cells. <i>Immunity</i> , 2022, 55, 98-114.e5.	6.6	38
610	Integration of single-cell transcriptomes and chromatin landscapes reveals regulatory programs driving pharyngeal organ development. <i>Nature Communications</i> , 2022, 13, 457.	5.8	22
611	Single-Cell RNA Sequencing Atlas From a Bivalve Larva Enhances Classical Cell Lineage Studies. <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	10
612	ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis. <i>Circulation</i> , 2022, 145, 469-485.	1.6	31
616	CellRank for directed single-cell fate mapping. <i>Nature Methods</i> , 2022, 19, 159-170.	9.0	286
617	Genome-wide association study on 13,167 individuals identifies regulators of blood CD34+ cell levels. <i>Blood</i> , 2022, 139, 1659-1669.	0.6	4
618	Deep structural clustering for single-cell RNA-seq data jointly through autoencoder and graph neural network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	22
619	Zero-preserving imputation of single-cell RNA-seq data. <i>Nature Communications</i> , 2022, 13, 192.	5.8	93
621	PanClassif: Improving pan cancer classification of single cell RNA-seq gene expression data using machine learning. <i>Genomics</i> , 2022, 114, 110264.	1.3	9
622	Statistics or biology: the zero-inflation controversy about scRNA-seq data. <i>Genome Biology</i> , 2022, 23, 31.	3.8	302
623	Single-Cell RNA-Seq Technologies and Computational Analysis Tools: Application in Cancer Research. <i>Methods in Molecular Biology</i> , 2022, 2413, 245-255.	0.4	2
624	Modeling uniquely human gene regulatory function via targeted humanization of the mouse genome. <i>Nature Communications</i> , 2022, 13, 304.	5.8	16

#	ARTICLE	IF	CITATIONS
625	Balancing Geometry and Density: Path Distances on High-Dimensional Data. <i>SIAM Journal on Mathematics of Data Science</i> , 2022, 4, 72-99.	1.0	3
626	A Bayesian factorization method to recover single-cell RNA sequencing data. <i>Cell Reports Methods</i> , 2022, 2, 100133.	1.4	4
627	MUC1-C integrates type II interferon and chromatin remodeling pathways in immunosuppression of prostate cancer. <i>Onc Immunology</i> , 2022, 11, 2029298.	2.1	17
629	Prdm6 controls heart development by regulating neural crest cell differentiation and migration. <i>JCI Insight</i> , 2022, 7, .	2.3	13
630	Effect of imputation on gene network reconstruction from single-cell RNA-seq data. <i>Patterns</i> , 2022, 3, 100414.	3.1	17
631	Network inference with Granger causality ensembles on single-cell transcriptomics. <i>Cell Reports</i> , 2022, 38, 110333.	2.9	53
632	Mouse genomic and cellular annotations. <i>Mammalian Genome</i> , 2022, 33, 19-30.	1.0	2
633	Systems-based approaches to study immunometabolism. <i>Cellular and Molecular Immunology</i> , 2022, 19, 409-420.	4.8	25
635	Time-restricted feeding prevents deleterious metabolic effects of circadian disruption through epigenetic control of I ² cell function. <i>Science Advances</i> , 2021, 7, eabg6856.	4.7	21
637	Allelic variation in class I HLA determines CD8 T cell repertoire shape and cross-reactive memory responses to SARS-CoV-2. <i>Science Immunology</i> , 2021, , eabk3070.	5.6	10
638	Network-based Structural Learning Nonnegative Matrix Factorization Algorithm for Clustering of scRNA-seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, PP, 1-1.	1.9	14
639	Dermal α 5 β 1 integrin myofibroblasts orchestrate skin wound repair via α 2 β 1 integrin and independent of type I collagen production. <i>EMBO Journal</i> , 2022, 41, e109470.	3.5	26
640	Perspectives on Bulk-Tissue RNA Sequencing and Single-Cell RNA Sequencing for Cardiac Transcriptomics. <i>Frontiers in Molecular Medicine</i> , 2022, 2, .	0.6	14
641	Multiscale PHATE identifies multimodal signatures of COVID-19. <i>Nature Biotechnology</i> , 2022, 40, 681-691.	9.4	39
643	IQCELL: A platform for predicting the effect of gene perturbations on developmental trajectories using single-cell RNA-seq data. <i>PLoS Computational Biology</i> , 2022, 18, e1009907.	1.5	13
645	A novel method for single-cell data imputation using subspace regression. <i>Scientific Reports</i> , 2022, 12, 2697.	1.6	6
647	A specialist-generalist framework for epithelial-mesenchymal plasticity in cancer. <i>Trends in Cancer</i> , 2022, 8, 358-368.	3.8	16
648	Regulatory network-based imputation of dropouts in single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009849.	1.5	5

#	ARTICLE	IF	CITATIONS
649	Deciphering endothelial heterogeneity in health and disease at single-cell resolution: progress and perspectives. <i>Cardiovascular Research</i> , 2023, 119, 6-27.	1.8	19
651	Guidelines for bioinformatics of single-cell sequencing data analysis in Alzheimer's disease: review, recommendation, implementation and application. <i>Molecular Neurodegeneration</i> , 2022, 17, 17.	4.4	40
654	ZFP541 maintains the repression of pre-pachytene transcriptional programs and promotes male meiosis progression. <i>Cell Reports</i> , 2022, 38, 110540.	2.9	11
657	DSAE-Impute: Learning Discriminative Stacked Autoencoders for Imputing Single-cell RNA-seq Data. <i>Current Bioinformatics</i> , 2022, 17, 440-451.	0.7	5
660	PHGDH is required for germinal center formation and is a therapeutic target in MYC-driven lymphoma. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	14
661	Sincast: a computational framework to predict cell identities in single-cell transcriptomes using bulk atlases as references. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
662	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. <i>Cell Genomics</i> , 2022, 2, 100107.	3.0	58
665	Integrating transcription-factor abundance with chromatin accessibility in human erythroid lineage commitment. <i>Cell Reports Methods</i> , 2022, 2, 100188.	1.4	9
666	Functional, metabolic and transcriptional maturation of human pancreatic islets derived from stem cells. <i>Nature Biotechnology</i> , 2022, 40, 1042-1055.	9.4	135
667	CD90 Marks a Mesenchymal Program in Human Thymic Epithelial Cells In Vitro and In Vivo. <i>Frontiers in Immunology</i> , 2022, 13, 846281.	2.2	5
668	Radiotherapy orchestrates natural killer cell dependent antitumor immune responses through CXCL8. <i>Science Advances</i> , 2022, 8, eabh4050.	4.7	55
671	A universal deep neural network for in-depth cleaning of single-cell RNA-Seq data. <i>Nature Communications</i> , 2022, 13, 1901.	5.8	15
672	Efficient differentiation of human primordial germ cells through geometric control reveals a key role for Nodal signaling. <i>ELife</i> , 2022, 11, .	2.8	24
673	SPCS: a spatial and pattern combined smoothing method for spatial transcriptomic expression. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
675	Lhx2 in germ cells suppresses endothelial cell migration in the developing ovary. <i>Experimental Cell Research</i> , 2022, 415, 113108.	1.2	8
676	Clustering single-cell RNA sequencing data by multi-view latent embedding learning. , 2021, , .		1
677	scIDS: Single-cell Imputation by combining Deep autoencoder neural networks and Subspace regression. , 2021, , .		0
678	Single-cell RNA sequencing data imputation using similarity preserving network. , 2021, , .		0

#	ARTICLE	IF	CITATIONS
679	Time-Series Analysis of Gene Correlation Networks based on Single-Cell Transcriptome Data. , 2021, , .		1
680	Immunosuppressive Traits of the Hybrid Epithelial/Mesenchymal Phenotype. <i>Frontiers in Immunology</i> , 2021, 12, 797261.	2.2	52
682	Interpretable network propagation with application to expanding the repertoire of human proteins that interact with SARS-CoV-2. <i>GigaScience</i> , 2021, 10, .	3.3	5
683	Intraperitoneal microbial contamination drives post-surgical peritoneal adhesions by mesothelial EGFR-signaling. <i>Nature Communications</i> , 2021, 12, 7316.	5.8	22
684	Lipid-loaded tumor-associated macrophages sustain tumor growth and invasiveness in prostate cancer. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	53
685	Deep learning tackles single-cell analysisâ€”a survey of deep learning for scRNA-seq analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	19
686	PPIL4 is essential for brain angiogenesis and implicated in intracranial aneurysms in humans. <i>Nature Medicine</i> , 2021, 27, 2165-2175.	15.2	23
689	MarkovHC: Markov hierarchical clustering for the topological structure of high-dimensional single-cell omics data with transition pathway and critical point detection. <i>Nucleic Acids Research</i> , 2022, 50, 46-56.	6.5	9
690	An efficient scRNA-seq dropout imputation method using graph attention network. <i>BMC Bioinformatics</i> , 2021, 22, 582.	1.2	5
692	MOJITOO: a fast and universal method for integration of multimodal single-cell data. <i>Bioinformatics</i> , 2022, 38, i282-i289.	1.8	6
693	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. <i>Nucleic Acids Research</i> , 2022, 50, 4877-4899.	6.5	12
694	Artificial intelligence in food science and nutrition: a narrative review. <i>Nutrition Reviews</i> , 2022, 80, 2288-2300.	2.6	22
695	scESI: evolutionary sparse imputation for single-cell transcriptomes from nearest neighbor cells. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
696	Identification of Functional Heterogeneity of Carcinoma-Associated Fibroblasts with Distinct IL6-Mediated Therapy Resistance in Pancreatic Cancer. <i>Cancer Discovery</i> , 2022, 12, 1580-1597.	7.7	100
697	mbDenoise: microbiome data denoising using zero-inflated probabilistic principal components analysis. <i>Genome Biology</i> , 2022, 23, 94.	3.8	8
698	SimiC enables the inference of complex gene regulatory dynamics across cell phenotypes. <i>Communications Biology</i> , 2022, 5, 351.	2.0	3
699	Progenitor potential of lung epithelial organoid cells in a transplantation model. <i>Cell Reports</i> , 2022, 39, 110662.	2.9	26
701	Single-cell transcriptomics identifies Mcl-1 as a target for senolytic therapy in cancer. <i>Nature Communications</i> , 2022, 13, 2177.	5.8	35

#	ARTICLE	IF	CITATIONS
702	Mapping human haematopoietic stem cells from haemogenic endothelium to birth. <i>Nature</i> , 2022, 604, 534-540.	13.7	88
722	Fast and robust imputation for miRNA expression data using constrained least squares. <i>BMC Bioinformatics</i> , 2022, 23, 145.	1.2	0
723	Dissection of the Differentiation of Human Monocyte Subtypes to Osteoclasts at Single-Cell Resolution. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
724	scTSSR2: Imputing Dropout Events for Single-Cell RNA Sequencing Using Fast Two-Side Self-Representation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1445-1456.	1.9	0
725	A Genetic Bottleneck of Mitochondrial DNA During Human Lymphocyte Development. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	18
726	Imputing dropouts for single-cell RNA sequencing based on multi-objective optimization. <i>Bioinformatics</i> , 2022, 38, 3222-3230.	1.8	5
729	Single-cell atlas of peripheral blood mononuclear cells from pregnant women. <i>Clinical and Translational Medicine</i> , 2022, 12, e821.	1.7	12
730	NISC: Neural Network-Imputation for Single-Cell RNA Sequencing and Cell Type Clustering. <i>Frontiers in Genetics</i> , 2022, 13, 847112.	1.1	4
731	Gene regulation by gonadal hormone receptors underlies brain sex differences. <i>Nature</i> , 2022, 606, 153-159.	13.7	71
732	Bringing machine learning to research on intellectual and developmental disabilities: taking inspiration from neurological diseases. <i>Journal of Neurodevelopmental Disorders</i> , 2022, 14, 28.	1.5	9
733	Statistical parametrization of cell cytoskeleton reveals lung cancer cytoskeletal phenotype with partial EMT signature. <i>Communications Biology</i> , 2022, 5, 407.	2.0	8
734	DAE-TPGM: A deep autoencoder network based on a two-part-gamma model for analyzing single-cell RNA-seq data. <i>Computers in Biology and Medicine</i> , 2022, 146, 105578.	3.9	1
735	Improvements Achieved by Multiple Imputation for Single-Cell RNA-Seq Data in Clustering Analysis and Differential Expression Analysis. <i>Journal of Computational Biology</i> , 2022, 29, 634-649.	0.8	5
736	Benchmarking spatial and single-cell transcriptomics integration methods for transcript distribution prediction and cell type deconvolution. <i>Nature Methods</i> , 2022, 19, 662-670.	9.0	130
737	Single-Cell Analysis of the Transcriptome and Epigenome. <i>Methods in Molecular Biology</i> , 2022, , 21-60.	0.4	5
740	Generation of specialized blood vessels via lymphatic transdifferentiation. <i>Nature</i> , 2022, 606, 570-575.	13.7	22
741	Tumor-induced erythroid precursor-differentiated myeloid cells mediate immunosuppression and curtail anti-PD-1/PD-L1 treatment efficacy. <i>Cancer Cell</i> , 2022, 40, 674-693.e7.	7.7	41
742	A human breast atlas integrating single-cell proteomics and transcriptomics. <i>Developmental Cell</i> , 2022, 57, 1400-1420.e7.	3.1	50

#	ARTICLE	IF	CITATIONS
743	Redox regulation by TXNRD3 during epididymal maturation underlies capacitation-associated mitochondrial activity and sperm motility in mice. <i>Journal of Biological Chemistry</i> , 2022, 298, 102077.	1.6	8
744	Chromatin accessibility analysis reveals regulatory dynamics and therapeutic relevance of Vogt-Koyanagi-Harada disease. <i>Communications Biology</i> , 2022, 5, .	2.0	4
746	BCL6-dependent TCF-1+ progenitor cells maintain effector and helper CD4+ T cell responses to persistent antigen. <i>Immunity</i> , 2022, 55, 1200-1215.e6.	6.6	30
749	Development and Characterization of a Mass Cytometry Panel for Detecting the Effect of Acute Doxorubicin Exposure on Murine Cardiac Non-myocytes. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 0, , .	1.5	1
750	Multiomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity. <i>Cell Systems</i> , 2022, 13, 598-614.e6.	2.9	10
751	Spectral clustering of single-cell multi-omics data on multilayer graphs. <i>Bioinformatics</i> , 2022, 38, 3600-3608.	1.8	3
752	Machine Learning: A Tool to Shape the Future of Medicine. <i>Studies in Big Data</i> , 2022, , 177-218.	0.8	2
754	Inference of cell state transitions and cell fate plasticity from single-cell with MARGARET. <i>Nucleic Acids Research</i> , 2022, 50, e86-e86.	6.5	6
755	Mapping Phenotypic Plasticity upon the Cancer Cell State Landscape Using Manifold Learning. <i>Cancer Discovery</i> , 2022, 12, 1847-1859.	7.7	26
756	CXCR4+ Treg cells control serum IgM levels and natural IgM autoantibody production by B-1 cells in the bone marrow. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	8
758	Dependence on the MUC1-C Oncoprotein in Classic, Variant, and Non-neuroendocrine Small Cell Lung Cancer. <i>Molecular Cancer Research</i> , 2022, 20, 1379-1390.	1.5	8
760	Genetic tracing reveals transcription factor Foxp3-dependent and Foxp3-independent functionality of peripherally induced Treg cells. <i>Immunity</i> , 2022, 55, 1173-1184.e7.	6.6	33
761	Morphological pseudotime ordering and fate mapping reveal diversification of cerebellar inhibitory interneurons. <i>Nature Communications</i> , 2022, 13, .	5.8	7
763	Benchmarking imputation methods for network inference using a novel method of synthetic scRNA-seq data generation. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	3
765	Mex3a marks drug-tolerant persister colorectal cancer cells that mediate relapse after chemotherapy. <i>Nature Cancer</i> , 2022, 3, 1052-1070.	5.7	36
767	Machine Learning Predictor of Immune Checkpoint Blockade Response in Gastric Cancer. <i>Cancers</i> , 2022, 14, 3191.	1.7	8
769	Mediators of Capillary-to-Venule Conversion in the Chronic Inflammatory Skin Disease Psoriasis. <i>Journal of Investigative Dermatology</i> , 2022, 142, 3313-3326.e13.	0.3	6
770	Tissue-resident memory CD8+ T cells possess unique transcriptional, epigenetic and functional adaptations to different tissue environments. <i>Nature Immunology</i> , 2022, 23, 1121-1131.	7.0	84

#	ARTICLE	IF	CITATIONS
771	Detection of cell markers from single cell RNA-seq with sc2marker. BMC Bioinformatics, 2022, 23, .	1.2	7
773	Approaches in Gene Coexpression Analysis in Eukaryotes. Biology, 2022, 11, 1019.	1.3	4
774	Missing Value Imputation With Low-Rank Matrix Completion in Single-Cell RNA-Seq Data by Considering Cell Heterogeneity. Frontiers in Genetics, 0, 13, .	1.1	2
775	CRISPR screening uncovers a central requirement for HHEX in pancreatic lineage commitment and plasticity restriction. Nature Cell Biology, 2022, 24, 1064-1076.	4.6	15
776	Single-cell network biology characterizes cell type gene regulation for drug repurposing and phenotype prediction in Alzheimer's disease. PLoS Computational Biology, 2022, 18, e1010287.	1.5	9
777	Multimodal Dimension Reduction and Subtype Classification of Head and Neck Squamous Cell Tumors. Frontiers in Oncology, 0, 12, .	1.3	2
778	A reference single-cell regulomic and transcriptomic map of cynomolgus monkeys. Nature Communications, 2022, 13, .	5.8	20
780	cclImpute: an accurate and scalable consensus clustering based algorithm to impute dropout events in the single-cell RNA-seq data. BMC Bioinformatics, 2022, 23, .	1.2	4
782	Transcriptional dynamics and epigenetic regulation of E and ID protein encoding genes during human T cell development. Frontiers in Immunology, 0, 13, .	2.2	4
785	scGENA: A Single-Cell Gene Coexpression Network Analysis Framework for Clustering Cell Types and Revealing Biological Mechanisms. Bioengineering, 2022, 9, 353.	1.6	5
786	Single-cell multimodal analysis identifies common regulatory programs in synovial fibroblasts of rheumatoid arthritis patients and modeled TNF-driven arthritis. Genome Medicine, 2022, 14, .	3.6	23
787	GE-Impute: graph embedding-based imputation for single-cell RNA-seq data. Briefings in Bioinformatics, 2022, 23, .	3.2	6
788	Claudin5 protects the peripheral endothelial barrier in an organ and vessel-type-specific manner. ELife, 0, 11, .	2.8	22
789	Inferring gene regulation from stochastic transcriptional variation across single cells at steady state. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	14
790	Single-cell RNA-sequencing identifies anti-cancer immune phenotypes in the early lung metastatic niche during breast cancer. Clinical and Experimental Metastasis, 2022, 39, 865-881.	1.7	6
791	scBasset: sequence-based modeling of single-cell ATAC-seq using convolutional neural networks. Nature Methods, 2022, 19, 1088-1096.	9.0	40
792	NetTIME: a Multitask and Base-pair Resolution Framework for Improved Transcription Factor Binding Site Prediction. Bioinformatics, 0, , .	1.8	1
793	Lineage plasticity in prostate cancer depends on JAK/STAT inflammatory signaling. Science, 2022, 377, 1180-1191.	6.0	92

#	ARTICLE	IF	CITATIONS
794	Single Cell Analysis Reveals Reciprocal Tumor-Macrophage Intercellular Communications Related with Metabolic Reprogramming in Stem-like Gastric Cancer. <i>Cells</i> , 2022, 11, 2373.	1.8	3
795	Metacells untangle large and complex single-cell transcriptome networks. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	14
796	Pancreas agenesis mutations disrupt a lead enhancer controlling a developmental enhancer cluster. <i>Developmental Cell</i> , 2022, 57, 1922-1936.e9.	3.1	8
797	Probabilistic boolean networks predict transcription factor targets to induce transdifferentiation. <i>IScience</i> , 2022, 25, 104951.	1.9	3
798	Resolution of the curse of dimensionality in single-cell RNA sequencing data analysis. <i>Life Science Alliance</i> , 2022, 5, e202201591.	1.3	7
800	Accurate inference of genome-wide spatial expression with iSpatial. <i>Science Advances</i> , 2022, 8, .	4.7	5
801	scWMC: weighted matrix completion-based imputation of scRNA-seq data via prior subspace information. <i>Bioinformatics</i> , 2022, 38, 4537-4545.	1.8	1
803	Phenotypic heterogeneity driven by plasticity of the intermediate EMT state governs disease progression and metastasis in breast cancer. <i>Science Advances</i> , 2022, 8, .	4.7	55
804	Competition between hematopoietic stem and progenitor cells controls hematopoietic stem cell compartment size. <i>Nature Communications</i> , 2022, 13, .	5.8	9
805	In search of a <i>Drosophila</i> core cellular network with single-cell transcriptome data. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	0
806	Archetype tasks link intratumoral heterogeneity to plasticity and cancer hallmarks in small cell lung cancer. <i>Cell Systems</i> , 2022, 13, 690-710.e17.	2.9	22
807	scMTD: a statistical multidimensional imputation method for single-cell RNA-seq data leveraging transcriptome dynamic information. <i>Cell and Bioscience</i> , 2022, 12, .	2.1	3
808	Single-cell multi-modal GAN reveals spatial patterns in single-cell data from triple-negative breast cancer. <i>Patterns</i> , 2022, 3, 100577.	3.1	5
810	Stability of scRNA-Seq Analysis Workflows is Susceptible to Preprocessing and is Mitigated by Regularized or Supervised Approaches. <i>Evolutionary Bioinformatics</i> , 2022, 18, 117693432211230.	0.6	0
811	scHOIS: Determining Cell Heterogeneity Through Hierarchical Clustering Based on Optimal Imputation Strategy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1431-1444.	1.9	0
813	Decoding brain memory formation by single-cell RNA sequencing. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
814	SCDD: a novel single-cell RNA-seq imputation method with diffusion and denoising. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
817	Metabolic collateral lethal target identification reveals MTHFD2 paralogue dependency in ovarian cancer. <i>Nature Metabolism</i> , 2022, 4, 1119-1137.	5.1	13

#	ARTICLE	IF	CITATIONS
818	Murine fetal bone marrow does not support functional hematopoietic stem and progenitor cells until birth. <i>Nature Communications</i> , 2022, 13, .	5.8	13
819	Self-supervised contrastive learning for integrative single cell RNA-seq data analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	23
820	Recent developments in application of single-cell RNA sequencing in the tumour immune microenvironment and cancer therapy. <i>Military Medical Research</i> , 2022, 9, .	1.9	19
822	Single-cell transcriptomics identifies conserved regulators of neuroglandular lineages. <i>Cell Reports</i> , 2022, 40, 111370.	2.9	34
823	IL1R2 increases regulatory T cell population in the tumor microenvironment by enhancing MHC-II expression on cancer-associated fibroblasts. , 2022, 10, e004585.		6
824	Therapeutic implications of mitochondrial stressâ€‘induced proteasome inhibitor resistance in multiple myeloma. <i>Science Advances</i> , 2022, 8, .	4.7	8
825	Novel antigen-presenting cell imparts Treg-dependent tolerance to gut microbiota. <i>Nature</i> , 2022, 610, 752-760.	13.7	78
826	Dysregulated stem cell niches and altered lymphocyte recirculation cause B and T cell lymphopenia in WHIM syndrome. <i>Science Immunology</i> , 2022, 7, .	5.6	9
827	From multitude to singularity: An up-to-date overview of scRNA-seq data generation and analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
829	Endothelial cell cycle state determines propensity for arterial-venous fate. <i>Nature Communications</i> , 2022, 13, .	5.8	22
830	Single-cell transcriptomics reveals functionally specialized vascular endothelium in brain. <i>ELife</i> , 0, 11, .	2.8	32
831	BATF epigenetically and transcriptionally controls the activation program of regulatory T cells in human tumors. <i>Science Immunology</i> , 2022, 7, .	5.6	23
832	scGNN 2.0: a graph neural network tool for imputation and clustering of single-cell RNA-Seq data. <i>Bioinformatics</i> , 2022, 38, 5322-5325.	1.8	8
833	MINI-EX: Integrative inference of single-cell gene regulatory networks in plants. <i>Molecular Plant</i> , 2022, 15, 1807-1824.	3.9	16
835	Deep learning of cross-species single-cell landscapes identifies conserved regulatory programs underlying cell types. <i>Nature Genetics</i> , 2022, 54, 1711-1720.	9.4	17
836	Combining denoising of RNA-seq data and flux balance analysis for cluster analysis of single cells. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	3
837	Divergent clonal differentiation trajectories of T cell exhaustion. <i>Nature Immunology</i> , 2022, 23, 1614-1627.	7.0	49
838	Development of Single-Cell Transcriptomics and Its Application in COVID-19. <i>Viruses</i> , 2022, 14, 2271.	1.5	1

#	ARTICLE	IF	CITATIONS
839	Single Cell Transcriptomics to Understand HSC Heterogeneity and Its Evolution upon Aging. <i>Cells</i> , 2022, 11, 3125.	1.8	2
840	Entropy sorting of single-cell RNA sequencing data reveals the inner cell mass in the human pre-implantation embryo. <i>Stem Cell Reports</i> , 2023, 18, 47-63.	2.3	17
841	The application of single-cell sequencing in pancreatic neoplasm: analysis, diagnosis and treatment. <i>British Journal of Cancer</i> , 2023, 128, 206-218.	2.9	2
842	AlscEA: unsupervised integration of single-cell gene expression and chromatin accessibility via their biological consistency. <i>Bioinformatics</i> , 0, , .	1.8	0
843	Interaction-based transcriptome analysis via differential network inference. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	1
844	Imputation Methods for scRNA Sequencing Data. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 10684.	1.3	3
849	AE-TPGG: a novel autoencoder-based approach for single-cell RNA-seq data imputation and dimensionality reduction. <i>Frontiers of Computer Science</i> , 2023, 17, .	1.6	5
851	Alignment of single-cell trajectory trees with CAPITAL. <i>Nature Communications</i> , 2022, 13, .	5.8	8
852	Single-cell and single-nuclei RNA sequencing as powerful tools to decipher cellular heterogeneity and dysregulation in neurodegenerative diseases. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	15
853	Single Cell Analysis of Gastric Cancer Reveals Non-Defined Telomere Maintenance Mechanism. <i>Cells</i> , 2022, 11, 3342.	1.8	3
854	PD-L1 Activity Is Associated with Partial EMT and Metabolic Reprogramming in Carcinomas. <i>Current Oncology</i> , 2022, 29, 8285-8301.	0.9	12
855	NF kappa B regulator Bcl3 controls development and function of classical dendritic cells required for resistance to <i>Toxoplasma gondii</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010502.	2.1	5
856	Protocol to dissociate, process, and analyze the human lung tissue using single-cell RNA-seq. <i>STAR Protocols</i> , 2022, 3, 101776.	0.5	4
857	Engineered exosomes targeting MYC reverse the proneural-mesenchymal transition and extend survival of glioblastoma. , 2022, 1, 100014.		10
858	Geometry Regularized Autoencoders. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2023, 45, 7381-7394.	9.7	3
859	Dynamic Graph Neural Network Learning for Temporal Omics Data Prediction. <i>IEEE Access</i> , 2022, 10, 116241-116252.	2.6	1
860	Region-specific denoising identifies spatial co-expression patterns and intra-tissue heterogeneity in spatially resolved transcriptomics data. <i>Nature Communications</i> , 2022, 13, .	5.8	4
861	Molecular Characterization of Acquired Resistance to KRASG12Câ€™EGFR Inhibition in Colorectal Cancer. <i>Cancer Discovery</i> , 2023, 13, 41-55.	7.7	25

#	ARTICLE	IF	CITATIONS
862	Gradual differentiation uncoupled from cell cycle exit generates heterogeneity in the epidermal stem cell layer. <i>Nature Cell Biology</i> , 2022, 24, 1692-1700.	4.6	24
863	Tumor suppressor DEAR1 regulates mammary epithelial cell fate and predicts early onset and metastasis in triple negative breast cancer. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
867	Metastatic recurrence in colorectal cancer arises from residual EMP1+ cells. <i>Nature</i> , 2022, 611, 603-613.	13.7	50
869	Alternative splicing downstream of EMT enhances phenotypic plasticity and malignant behavior in colon cancer. <i>ELife</i> , 0, 11, .	2.8	5
872	scBKAP: A Clustering Model for Single-Cell RNA-Seq Data Based on Bisecting K-Means. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 2007-2015.	1.9	3
873	Computational and Statistical Methods for Single-Cell RNA Sequencing Data. <i>Springer Handbooks of Computational Statistics</i> , 2022, , 3-35.	0.2	0
874	scDrug: From single-cell RNA-seq to drug response prediction. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 150-157.	1.9	9
875	Pathway trajectory analysis with tensor imputation reveals drug-induced single-cell transcriptomic landscape. <i>Nature Computational Science</i> , 2022, 2, 758-770.	3.8	1
876	Estimating Metastatic Risk of Pancreatic Ductal Adenocarcinoma at Single-Cell Resolution. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15020.	1.8	0
879	Leveraging data-driven self-consistency for high-fidelity gene expression recovery. <i>Nature Communications</i> , 2022, 13, .	5.8	4
881	Data analysis guidelines for single-cell RNA-seq in biomedical studies and clinical applications. <i>Military Medical Research</i> , 2022, 9, .	1.9	4
882	An NKX-COUP-TFI morphogenetic code directs mucosal endothelial addressin expression. <i>Nature Communications</i> , 2022, 13, .	5.8	4
884	Single-Cell RNAseq Data QC and Preprocessing. <i>Methods in Molecular Biology</i> , 2023, , 205-215.	0.4	0
886	Application of Deep Learning on Single-cell RNA Sequencing Data Analysis: A Review. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 814-835.	3.0	15
887	IL7 genetic variation and toxicity to immune checkpoint blockade in patients with melanoma. <i>Nature Medicine</i> , 2022, 28, 2592-2600.	15.2	22
888	Quantification of extracellular proteins, protein complexes and mRNAs in single cells by proximity sequencing. <i>Nature Methods</i> , 2022, 19, 1578-1589.	9.0	9
889	Single-cell RNA sequencing provides a high-resolution roadmap for understanding the multicellular compartmentation of specialized metabolism. <i>Nature Plants</i> , 2023, 9, 179-190.	4.7	32
891	Computational Methods for Single-cell Multi-omics Integration and Alignment. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 836-849.	3.0	23

#	ARTICLE	IF	CITATIONS
892	Bubble: a fast single-cell RNA-seq imputation using an autoencoder constrained by bulk RNA-seq data. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	5
895	Macrophage inflammatory and regenerative response periodicity is programmed by cell cycle and chromatin state. <i>Molecular Cell</i> , 2023, 83, 121-138.e7.	4.5	11
897	Single-cell RNA-seq data analysis using graph autoencoders and graph attention networks. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
898	A Framework for Comparison and Assessment of Synthetic RNA-Seq Data. <i>Genes</i> , 2022, 13, 2362.	1.0	3
900	Trends and Potential of Machine Learning and Deep Learning in Drug Study at Single-Cell Level. <i>Research</i> , 2023, 6, .	2.8	10
902	Identifying strengths and weaknesses of methods for computational network inference from single-cell RNA-seq data. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	12
905	Chemotherapy-induced tumor immunogenicity is mediated in part by megakaryocyte-erythroid progenitors. <i>Oncogene</i> , 2023, 42, 771-781.	2.6	2
906	Integrated single-cell profiling dissects cell-state-specific enhancer landscapes of human tumor-infiltrating CD8+ T cells. <i>Molecular Cell</i> , 2023, 83, 622-636.e10.	4.5	7
907	Using Single-Cell RNA Sequencing and MicroRNA Targeting Data to Improve Colorectal Cancer Survival Prediction. <i>Cells</i> , 2023, 12, 228.	1.8	5
908	Graph embedding and Gaussian mixture variational autoencoder network for end-to-end analysis of single-cell RNA sequencing data. <i>Cell Reports Methods</i> , 2023, 3, 100382.	1.4	21
910	sclAC: clustering scATAC-seq data based on Student's t-distribution similarity imputation and denoising autoencoder. , 2022, , .		2
911	scSASSL: Self-attention semi-supervised learning with deep generative models to automatically identify cell types. , 2022, , .		0
912	Machine learning development environment for single-cell sequencing data analyses. , 2022, , .		0
914	SCdenoise: a reference-based scRNA-seq denoising method using semi-supervised learning. , 2022, , .		0
915	The actin cytoskeleton: Morphological changes in pre- and fully developed lung cancer. <i>Biophysics Reviews</i> , 2022, 3, 041304.	1.0	0
916	Improved downstream functional analysis of single-cell RNA-sequence data using DGAN. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
917	SMURF: embedding single-cell RNA-seq data with matrix factorization preserving self-consistency. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	1
919	Key transcription factors influence the epigenetic landscape to regulate retinal cell differentiation. <i>Nucleic Acids Research</i> , 2023, 51, 2151-2176.	6.5	4

#	ARTICLE	IF	CITATIONS
923	scRNA-seq data analysis method to improve analysis performance. IET Nanobiotechnology, 2023, 17, 246-256.	1.9	5
924	Quantitative analysis of high-throughput biological data. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2023, 13, .	6.2	2
925	Characterization of altered molecular mechanisms in Parkinson's disease through cell type-resolved multiomics analyses. Science Advances, 2023, 9, .	4.7	11
926	ETV4 mediates dosage-dependent prostate tumor initiation and cooperates with p53 loss to generate prostate cancer. Science Advances, 2023, 9, .	4.7	2
927	KGLRR: A low-rank representation K-means with graph regularization constraint method for Single-cell type identification. Computational Biology and Chemistry, 2023, 104, 107862.	1.1	1
928	Transcriptional networks of transient cell states during human prefrontal cortex development. Frontiers in Molecular Neuroscience, 0, 16, .	1.4	0
930	Stepwise fate conversion of supporting cells to sensory hair cells in the chick auditory epithelium. IScience, 2023, 26, 106046.	1.9	6
931	Three-dimensional chromatin reorganization during muscle stem cell aging. Aging Cell, 2023, 22, .	3.0	5
932	Chemical reprogramming of melanocytes to skeletal muscle cells. Journal of Cachexia, Sarcopenia and Muscle, 2023, 14, 903-914.	2.9	2
933	scGGAN: single-cell RNA-seq imputation by graph-based generative adversarial network. Briefings in Bioinformatics, 2023, 24, .	3.2	9
937	Unsupervised Diffusion and Volume Maximization-Based Clustering of Hyperspectral Images. Remote Sensing, 2023, 15, 1053.	1.8	1
938	Single-cell RNA-seq data analysis based on directed graph neural network. Methods, 2023, 211, 48-60.	1.9	2
940	scTSSR-D: Gene Expression Recovery by Two-side Self-representation and Dropout Information for scRNA-seq Data. Current Bioinformatics, 2023, 18, .	0.7	0
941	scSTAR reveals hidden heterogeneity with a real-virtual cell pair structure across conditions in single-cell RNA sequencing data. Briefings in Bioinformatics, 2023, 24, .	3.2	2
942	scGCL: an imputation method for scRNA-seq data based on graph contrastive learning. Bioinformatics, 2023, 39, .	1.8	4
943	Involvement of Epithelial-Mesenchymal Transition Genes in Small Cell Lung Cancer Phenotypic Plasticity. Cancers, 2023, 15, 1477.	1.7	4
944	A Unified Deep Learning Framework for Single-Cell ATAC-Seq Analysis Based on ProdDep Transformer Encoder. International Journal of Molecular Sciences, 2023, 24, 4784.	1.8	1
945	The ELF3 transcription factor is associated with an epithelial phenotype and represses epithelial-mesenchymal transition. Journal of Biological Engineering, 2023, 17, .	2.0	7

#	ARTICLE	IF	CITATIONS
947	Microenvironment-Driven Dynamic Chromatin Changes in Glioblastoma Recapitulate Early Neural Development at Single-Cell Resolution. <i>Cancer Research</i> , 2023, 83, 1581-1595.	0.4	3
948	Dynamic interplay between RPL3- and RPL3L-containing ribosomes modulates mitochondrial activity in the mammalian heart. <i>Nucleic Acids Research</i> , 2023, 51, 5301-5324.	6.5	13
951	A universal framework for single-cell multi-omics data integration with graph convolutional networks. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	7
953	Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Mouse Corneal Epithelial Cells. , 2023, 64, 30.		1
954	Imputation of single-cell transcriptome data enables the reconstruction of networks predictive of breast cancer metastasis. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2296-2304.	1.9	0
955	Pan-cancer classification of single cells in the tumour microenvironment. <i>Nature Communications</i> , 2023, 14, .	5.8	6
957	SEACells infers transcriptional and epigenomic cellular states from single-cell genomics data. <i>Nature Biotechnology</i> , 2023, 41, 1746-1757.	9.4	30
959	Epi-Impute: Single-Cell RNA-seq Imputation via Integration with Single-Cell ATAC-seq. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6229.	1.8	5
960	CD226 identifies functional CD8+T cells in the tumor microenvironment and predicts a better outcome for human gastric cancer. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
962	Identification of HPV16 E1 and E2-specific T cells in the oropharyngeal cancer tumor microenvironment. , 2023, 11, e006721.		3
964	Best practices for single-cell analysis across modalities. <i>Nature Reviews Genetics</i> , 2023, 24, 550-572.	7.7	128
965	NK-like CD8 ⁺ T cells are expanded in persistent <i>Mycobacterium tuberculosis</i> infection. <i>Science Immunology</i> , 2023, 8, .	5.6	9
966	Epicardioid single-cell genomics uncovers principles of human epicardium biology in heart development and disease. <i>Nature Biotechnology</i> , 2023, 41, 1787-1800.	9.4	10
968	A Scd1-mediated metabolic alteration participates in liver responses to low-dose bavachin. <i>Journal of Pharmaceutical Analysis</i> , 2023, 13, 806-816.	2.4	3
969	Hic1 identifies a specialized mesenchymal progenitor population in the embryonic limb responsible for bone superstructure formation. <i>Cell Reports</i> , 2023, 42, 112325.	2.9	0
970	A single-cell, time-resolved profiling of <i>Xenopus</i> mucociliary epithelium reveals nonhierarchical model of development. <i>Science Advances</i> , 2023, 9, .	4.7	3
972	DNA architectural protein CTCF facilitates subset-specific chromatin interactions to limit the formation of memory CD8+ T cells. <i>Immunity</i> , 2023, 56, 959-978.e10.	6.6	5
974	Accurate and interpretable gene expression imputation on scRNA-seq data using IGSimpute. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	2

#	ARTICLE	IF	CITATIONS
975	Pleiotropic role of TRAF7 in skull-base meningiomas and congenital heart disease. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	4
976	A systems biology approach uncovers novel disease mechanisms in age-related macular degeneration. Cell Genomics, 2023, 3, 100302.	3.0	6
977	HSV-2 triggers upregulation of MALAT1 in CD4+ T cells and promotes HIV latency reversal. Journal of Clinical Investigation, 2023, 133, .	3.9	2
978	Single-nucleus RNA-sequencing of autosomal dominant Alzheimer disease and risk variant carriers. Nature Communications, 2023, 14, .	5.8	17
979	Allogeneic chimeric antigen receptor-T cells with CRISPR-disrupted programmed death-1 checkpoint exhibit enhanced functional fitness. Cytotherapy, 2023, 25, 750-762.	0.3	4
980	Single-cell analyses reveal cannabidiol rewires tumor microenvironment via inhibiting alternative activation of macrophage and synergizes with anti-PD-1 in colon cancer. Journal of Pharmaceutical Analysis, 2023, 13, 726-744.	2.4	5
984	Unraveling non-genetic heterogeneity in cancer with dynamical models and computational tools. Nature Computational Science, 2023, 3, 301-313.	3.8	7
990	Single-cell and spatial transcriptomics: deciphering brain complexity in health and disease. Nature Reviews Neurology, 2023, 19, 346-362.	4.9	33
993	Transcriptomic identification of cell types in the lower urinary tract. , 2023, , 159-166.		0
994	Diffusion Maps: Using the Semigroup Property for Parameter Tuning. Applied and Numerical Harmonic Analysis, 2023, , 409-424.	0.1	1
1024	Gene regulatory network inference in the era of single-cell multi-omics. Nature Reviews Genetics, 2023, 24, 739-754.	7.7	40
1060	Scientific discovery in the age of artificial intelligence. Nature, 2023, 620, 47-60.	13.7	113
1074	Sequencing-based methods for single-cell multi-omics studies. Science China Chemistry, 0, , .	4.2	0
1091	Gene regulatory network reconstruction: harnessing the power of single-cell multi-omic data. Npj Systems Biology and Applications, 2023, 9, .	1.4	2
1104	Diffusion models in bioinformatics and computational biology. , 2024, 2, 136-154.		3
1113	Data Imputation with an Autoencoder and MAGIC. , 2023, , .		0
1114	A Convergence Rate for Manifold Neural Networks. , 2023, , .		0
1138	Markov Matrix-based Kernel Reconstruction Method for PET Images. , 2023, , .		0

#	ARTICLE	IF	CITATIONS
1140	Single-cell transcriptomics in tissue engineering and regenerative medicine. , 2024, 2, 101-119.		0
1158	Application of machine learningâ€‘based approaches in stem cell research. , 2024, , 65-76.		0